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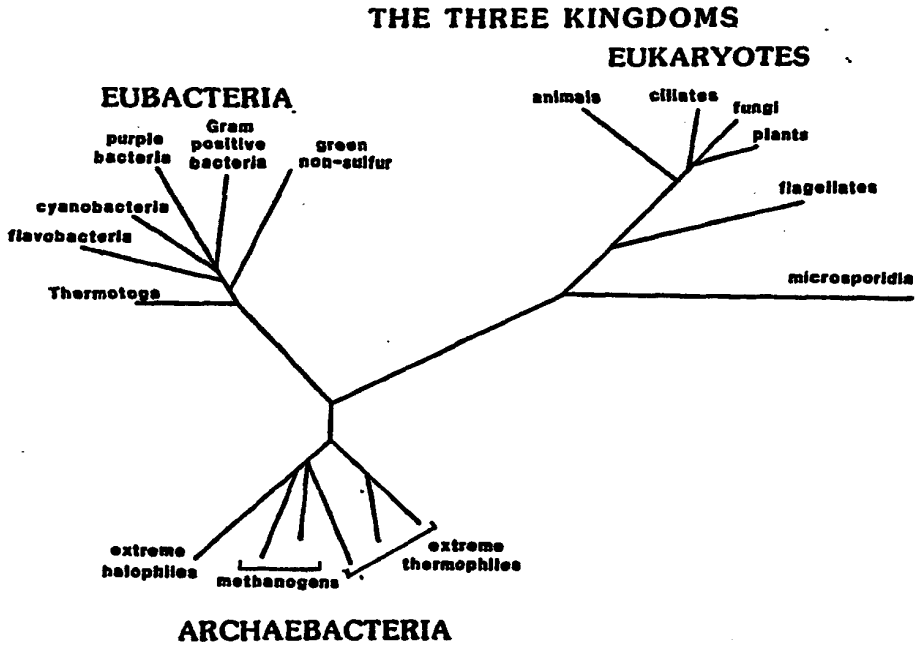

(57) Abstract

Nucleic acid probes capable of hybridizing to rRNA of eubacteria and not to rRNA of non-eubacteria are described along with methods utilizing such probes for the detection of eubacteria in clinical and other samples. Preferred embodiments include probes capable of distinguishing between gram-positive and gram-negative bacteria.

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UNIVERSAL EUBACTERIA NUCLEIC ACID PROBES AND METHODS

Field of the Invention

This invention relates to detection of bacteria in clinical and other samples. Methods for the detection of bacteria in ordinarily aseptic bodily tissues or fluids such as blood, urine, and cerebrospinal fluid fluid - where the presence of any bacterium may be life threatening are of particular importance. The present invention provides nucleic acid probes and compositions along with methods for their use for the specific detection of any bacterium in such samples.

Background of the Invention

The term "eubacteria" as used herein, refers to the group of prokaryotic organisms (bacteria) as described in, for example, Bergey's Manual of Systematic Bacteriology (N.R. Krieg and J.G. Holt, ed., 1984, Villiams & Wilkins, Baltimore). As a group, the eubacteria comprise all of the bacteria which are known to cause disease in humans or animals and are of most concern with respect to detection.

The only other described group of bacteria, the archaebacteria, are biologically and genetically distinct from the eubacteria (C.R. Woese, Scientific American, 1981, Volume 244, pages 98-102). Archaebacteria as a group occupy a variety of "extreme" environments such as hot springs, strongly oxygen-depleted muds, salt brines, etc., which generally do not support the growth of eubacteria. There are no known archaebacterial pathogens and, consequently, their detection is of little clinical significance.

Eukaryotic organisms comprise the third fundamental genetic lineage which, together with the eubacteria and archaebacteria, include all known life forms (Figure 1). Eukaryotes include humans, animals, plants and a host of organizationally less complex, free-living and parasitic "protists," including: protozoans, fungi, ciliates, etc. In a clinical context, it is particularly important that eubacteria be distinguished from eukaryotic, e.g. fungal and protozoan, infections which may present the same symptoms but require a significantly different regime of antimicrobial or chemo-therapy. These genetic distinctions thus are clinically significant from the point of view of diagnosis and antimicrobial chemotherapy.

It is an aspect of the present invention to provide nucleic acid probes which discriminate between eubacterial, human (including human mitochondrial) and fungal rRNA molecules.

It is another aspect of the present invention to provide probes and probe sets which provide a basis for discriminating between Gram positive and Gram negative eubacteria.

Methods for detecting, identifying and enumerating bacteria in normally sterile body fluids vary with the type of sample and the suspected pathogen. No currently available method is optimal for the detection of all pathogens. Often a combination of methods must be used to increase the likelihood that the pathogen will be detected. All commonly used methods for detection of, for example, bacteremia or bacterial septicemia rely on the in vitro cultivation of microbes from clinical samples. Generally, a blood sample is drawn from a patient and incubated in a rich artificial culture medium and monitored for 1 to 14 days. During this time, the medium is examined or blindly sub-cultured (plated), or assayed chemically or isotopically for evidence of bacterial growth or fermentative processes. Clinicians generally draw two or three samples of 10 milliliters of blood which may yield as

few as one to ten colony forming units of bacteria for a positive diagnosis. Following the isolation of individual colonies of bacteria on diagnostic solid media and/or by Gram-staining, presumptive identification of the bacteria (or fungus) is made.

All cultivation methods suffer a number of serious shortcomings, including the following:

- High material costs;
- Labor intensive;
- Technologists extensively handle dangerous bodily fluids;
- False positives due to handling;
- False negatives due to low viable cell numbers;
- False negatives due to fastidious media requirements of many potential pathogens; and
- Relatively long time to positive diagnosis and identification.

Because of the relatively long time required by current methods to achieve a diagnosis and because of the potentially life threatening nature of such infections, antimicrobial therapy often is begun empirically before the results of such tests can be known.

Therefore, it is another aspect of the present invention to provide nucleic acid probes which are broadly specific for all eubacteria and which preferably do not react with other eukaryotic pathogens, especially fungi, which may be present in sampled materials.

It is yet another aspect of the present invention to provide probes which may be used in a variety of assay systems which avoid many of the disadvantages associated with traditional, multi-day culturing techniques.

It is still another aspect of the present invention to provide probes that are capable of hybridizing to the ribosomal ribonucleic acid (rRNA) of the targeted eubacterial organisms under normal assay conditions.

While Kohne et al. (Biophysical Journal 8:1104-1118, 1968) discuss one method for preparing probes to rRNA sequences, they do not provide the teaching necessary to make broad-specificity eubacterial probes.

Pace and Campbell (Journal of Bacteriology 107:543-547, 1971) discuss the homology of ribosomal ribonucleic acids from diverse bacterial species and a hybridization method for quantitating such homology levels. They do not identify particular nucleic acid sequences shared by bacteria, but absent in eukaryotes. Woese (Microbiological Reviews 51:221-271, 1987) describes the breadth of the eubacteria, in terms of rRNA sequence, but does not indicate sequences of interest for complete bacterial inclusivity. These references, however, fail to relieve the deficiency of Kohne's teaching with respect to eubacterial probes and, in particular, do not provide eubacterial specific probes useful in assays for detecting eubacteria in clinical or other samples.

Giovannoni et al. (Journal of Bacteriology 170:720-726, 1988) describe a number of probes which are claimed to be useful for the identification of broad groups of eubacteria, archaebacteria and eukaryotes. However, Giovannoni et al. do not disclose the probes of the present invention. Nor do they provide the teaching necessary to design such probes.

Hogan et al. (European patent publication WO 88/03957) describe a number of probes which are claimed to hybridize to a broad representation of eubacteria. However, Hogan et al. do not teach the probes of the present invention and also fail to relieve the deficiency of Kohne's teaching with respect to these probes.

Ribosomes are of profound importance to all organisms because they serve as the only means of translating genetic information into cellular proteins. A clear manifestation of this importance is the observation that all cells have ribosomes. Actively growing bacteria may have 20,000 or more ribosomes per cell. This makes ribosomes one of the most abundant macromolecular entities in a cell, and an attractive diagnostic assay target.

Ribosomes contain three distinct RNA molecules which in Escherichia coli are referred to as 5S, 16S and 23S rRNAs. These names historically are related to the size of the RNA molecules, as determined by their sedimentation rate. In actuality, however, ribosomal RNA molecules vary in size between organisms. Nonetheless, 5S, 16S, and 23S rRNA are commonly used as generic names for the homologous RNA molecules in any bacteria, and this convention will be continued herein. Discussion will be confined to 16S and 23S rRNAs.

As used herein, probe(s) refer to synthetic or biologically produced nucleic acids (DNA or RNA) which, by design or selection, contain specific nucleotide sequences that allow them to hybridize under defined predetermined stringencies, specifically (i.e., preferentially, see below - Hybridization) to target nucleic acid sequences. In addition to their hybridization properties, probes also may contain certain constituents that pertain to their proper or optimal functioning under particular assay conditions. For example, probes may be modified to improve their resistance to nuclease degradation (e.g. by end capping), to carry detection ligands (e.g. fluorescein, 32-Phosphorous, biotin, etc.), or to facilitate their capture onto a solid

support (e. g., poly-deoxyadenosine "tails"). Such modifications are elaborations on the basic probe function which is its ability to usefully discriminate between target and non-target organisms in a hybridization assay.

Hybridization traditionally is understood as the process by which, under predetermined reaction conditions, two partially or completely complementary strands of nucleic acid are allowed to come together in an antiparallel fashion (one oriented 5′ to 3′, the other 3′ to 5′) to form a double-stranded nucleic acid with specific and stable hydrogen bonds. (Note that nucleic acids do have a polarity; that is, one end of a nucleic acid strand is chemically different from another. This is defined by the polarity of the chemical linkages through the asymmetric sugar moiety of the nucleotide components. The terms 5′ and 3′ specifically refer to the ribose sugar carbons which bear those names. Except in rare or unusual circumstances, nucleic acid strands do not associate through hydrogen bonding of the base moieties in a parallel fashion. This concept is well understood by those skilled in the art.)

The stringency of a particular set of hybridization conditions is defined by the base composition of the probe/target duplex, as well as by the level and geometry of mispairing between the two nucleic acids.

Stringency may also be governed by such reaction parameters as the concentration and type of ionic species present in the hybridization solution, the types and concentrations of denaturing agents present, and/or the temperature of hybridization. Generally, as hybridization conditions become more stringent, longer probes are preferred if stable hybrids are to be formed. As a corollary, the stringency of the conditions under which a hybridization is to take place (e. g., based on the type of assay to be performed) will dictate certain characteristics of the preferred probes to be employed. Such relationships are well understood and can be readily manipulated by those skilled in the art.

As a general matter, dependent upon probe length, such persons understand stringent conditions to mean approximately 35°C-65°C in a salt solution of approximately 0.9 molar.

Summary of the Invention

In accordance with the various principles and aspects of the present invention, there are provided nucleic acid probes and probe sets comprising deoxyribonucleic acid (DNA) or ribonucleic acid (RNA) sequences which hybridize, under specific conditions, to the ribosomal RNA molecules (rRNA), rRNA genes (rDNA), and certain amplification and in vitro transcription products thereof of eubacteria but which do not hybridize, under the same conditions, to the rRNA or rDNA of eukaryotic cells which may be present in test samples. In addition, certain of the probes and probe sets described herein may be used as primers for the specific amplification of eubacterial rRNA or rDNA sequences which may be present in a sample by such methods as the polymerase chain reaction (US 4,683,202) or transcriptional amplification systems (e.g. TAS, Kwoh et al., 1989, Proceedings of the National Academy of Science 86:1173-1177).

The probes of the present invention advantageously provide the basis for development of valuable nucleic acid hybridization assays for the specific detection of eubacteria in clinical samples such as blood, urine, cerebrospinal fluid, biopsy, synovial fluid, or other tissue or fluid samples from humans or animals. The probes also provide the basis for testing, for example in quality control, substances that are presumed sterile, e.g., pharmaceuticals. The probes described herein are specifically complimentary to certain highly conserved bacterial 23S or 16S rRNA sequences.

The detection of bacteria by nucleic acid hybridization constitutes enhanced performance capability compared to the available culture-dependent tests for several reasons including:

a) increased sensitivity; i.e., the ability to detect said bacteria in a given sample more frequently;

b) potentially significant reductions in assay cost due to the use of inexpensive reagents and reduced labor;

c) accurate detection of even nutritionally fastidious strains of bacteria;

d) faster results because such tests do not require the isolation of the target bacterium from the sample prior to testing;

e) the ability to screen, in a batch mode, a large number of samples, and only culture those identified as "hybridization positive";

f) potential detection of phagocytized organisms eliminating the need for multiple, punctuated blood samples in order to sample the cyclical "window" of viable organisms (which probably depends on host immunological cycles);

g) some reduction of technologist handling of potentially infectious body fluids;

h) the ability to detect very low numbers of targets by amplifying either the bacterial signal or target using <u>in vitro</u> nucleic acid amplification.

It has been discovered that other advantages incurred by directing the probes of the present invention against rRNA include the fact that the rRNAs detected constitute a significant component of cellular mass. Although estimates of cellular ribosome content vary, actively growing Escherichia coli, for example, may contain upwards of 50,000 ribosomes per cell, and therefore 50,000 copies of each of the rRNAs (present in a 1:1:1 stiochiometry in ribosomes). The abundance of ribosomes in other bacteria particularly under other, less favorable, metabolic conditions may be considerably lower. However, under any circumstances, rRNAs are among the most abundant cellular nucleic acids present in all cell types. In contrast, other potential cellular target molecules such as genes or RNA transcripts thereof, are less ideal since they are present in much lower abundance.

A further unexpected advantage is that the rRNAs (and the genes specifying them) appear not to be subject to lateral transfer between contemporary organisms. Thus, the rRNA primary structure provides an organism-specific molecular target, rather than a gene-specific target as would likely be the case, for example of a plasmid-borne gene or product thereof which may be subject to lateral transmission between contemporary organisms.

Additionally, the present invention provides probes to eubacterial rRNA target sequences which are sufficiently similar in most or all eubacteria tested that they can hybridize to the target region in such eubacteria. Advantageously, these same rRNA target sequences are sufficiently different in most non-eubacterial rRNAs that, under conditions where the probes hybridize to eubacterial rRNAs they do not hybridize to most non-eubacterial rRNAs. These probe characteristics are defined as inclusivity and exclusivity, respectively.

The discovery that probes could be generated with the extraordinary inclusivity and exclusivity characteristics of those of the present invention with respect to eubacteria was unpredictable and unexpected.

Brief Description of the Figures

Further understanding of the principles and aspects of the present invention may be made by reference to the tables wherein:

Figure 1 - Shows an evolutionary "tree" of the major genetic "kingdoms" of life (Woese, 1987, Microbiological Reviews 51:221- 271). The branching patterns represent the mutational distances between the 16S rRNA sequences of the represented organism. Such comparisons readily distinguish the eubacteria from the archaebacteria and eukaryotes.

Figure 2 - Shows a more detailed evolutionary tree of the eubacterial kingdom (ibid.). So far about 10 major divisions/phyla have been defined based on 16S rRNA sequence comparisons. Certain discriminations among eubacterial divisions can be important in a clinical context and certain of the probes of the present invention do exhibit preferential hybridization to one or more or the eubacterial divisions. Therefore, the test organisms listed in Tables 3, 4 and 5 are grouped according to the divisions shown in Figure 2 so that significant patterns of hybridization may be most easily discerned.

Brief Description of the Tables

Table 1 - Shows alignment of the nucleotide sequences of the preferred 16S rRNA-targeted probes of the present invention with their target nucleotide sequences in E. coli 16S rRNA. Very extensive sequence comparison to some 350 aligned 16S and 18S rRNA sequences were performed during the development of the probes of the present invention. It simply is not practical to show this analysis in detail. However, a consensus sequence (CONS-90%) of highly conserved 16S rRNA nucleotide positions is provided as a summary of the patterns of

nucleotide sequence variation discovered among representative eubacteria. A nucleotide on the CONS-90% line indicates that that nucleotide is found at the homologous position in 90% or greater of the eubacterial sequences inspected. Note that the probe target regions all correspond to clusters of high sequence conservation among the eubacterial 16S and 23S rRNA molecules.

Since the E. coli 16S and 23S rRNA sequences were among the first full rRNA sequences obtained, the assigned position numbers have become a convenient and commonly accepted standard for explicitly identifying the homologous regions in other rRNA sequences under consideration. In Table 1, the E. coli RNA (target) sequence is written 5′ to 3′. Probe sequences are DNA and written 3′ to 5′, except for probes 1638, 1642 and 1643 which are designed to hybridize to the rRNA-complementary sequence rather than the rRNA itself. These latter probes have the same "sense" (i. e. polarity) as the rRNA and are written 5′ to 3′.

Table 2 - Shows alignment of the nucleotide sequences of the preferred 23S rRNA-targeted probes of the present invention with their target nucleotide sequences in E. coli 23S rRNA. As in Table 1 the E. coli sequence numbering is used as a standard in order to identify the homologous probe target sequences in all 23S rRNAs. CONS-90% has the same meaning as in TABLE 1. For the 23S rRNA analyses only about 30 sequences were available. However, these represent most of the major eubacterial divisions shown in Figure 2. In the probe 1730 sequence, "R" = a 1:1 mixture of A and G at that position.

Table 3 - Exemplifies the inclusivity and exclusivity behavior of a number of the preferred 16S rRNA-targeted probes toward a representative sampling of eubacterial and non-eubacterial rRNAs in a dot blot hybridization assay.

Table 4 - Exemplifies the inclusivity and exclusivity behavior of a number of the preferred 23S rRNA-targeted probes toward a representative sampling of eubacterial and non-eubacterial rRNAs in a dot blot hybridization assay.

Table 5 - Exemplifies the inclusivity and exclusivity behavior of a number of additional preferred 16S and 23S rRNA-targeted probes toward a representative sampling of eubacterial and non-eubacterial rRNAs in a dot blot hybridization assay. These probes exhibit useful patterns of hybridization to specific subgroups of eubacteria - notably Gram positive and Gram negative bacteria.

Detailed Description of the Invention and Best Mode

Probe Development Strategy:

The first step taken in the development of the probes of the present invention involved identification of regions of 16S and 23S rRNA which potentially could serve as target sites for eubacteria specific nucleic acid probes. This entailed finding sites which are:

1) highly conserved (few nucleotide changes, deletions, or insertions) among eubacterial rRNA sequences, and

2) substantially different in non-eubacterial rRNA sequences.

For this analysis, precise alignments of available 16S and 23S rRNA sequences were developed. A number of 16S and 23S rRNA sequences were determined as part of this effort. Such nucleotide sequences were determined by standard laboratory protocols either by cloning (Maniatis et al., 1982, Molecular Cloning; A Laboratory Manual, Cold Spring Harbor Laboratory, New York, pp 545) and sequencing (Maxam and Gilbert,

1977, Proceedings of the National Academy of Science, USA 74:560-564: Sanger et al., 1977, Proceedings of the National Academy of Science, USA 74:5463-5467) the genes which specify the rRNAs, and/or by direct sequencing of the rRNAs themselves using reverse transcriptase (Lane et al., 1985, Proceedings of the National Academy of Science, USA 82:6955-6959; Lane, manuscript in preparation).

A computer algorithm, operating on the aligned set of 16S and 23S rRNA sequences, was used to identify regions of greatest similarity among eubacteria. Nucleic acid probes to such regions will hybridize most widely among diverse eubacteria.

Such regions of homology among eubacteria next were assessed for differences with non-eubacterial rRNA sequences. In particular, sequence differences between eubacterial and human, fungal, and mitochondrial sequences were sought.

Forty one probes were designed based on these analyses; 22 targeting 23S rRNA and 19 targeting 16S rRNA.

The hybridization behavior of these probes toward extensive panels of eubacteria was determined by hybridization analysis in a dot blot format.

Physical Description of the Probes:

The foregoing probe selection strategy yielded a number of probes useful for identifying eubacteria in samples and include the following preferred oligonucleotide probes:

16S rRNA-targeted probes:

Probe 1638: 5'-AGAGTTTGATCCTGGCTCAG-3'

Probe 1642: 5'-AGAGTTTGATCATGGCTCAG-3'

Probe 1643: 5'-AGAGTTTGATCCTGGCTTAG-3'

Probe 1738: 5'-CTGAGCCAGGATCAAACTCT-3'

Probe 1744: 5'-CAGCGTTCGTCCTGAGCCAGGATCAAACT-3'

Probe 1659: 5'-CTGCTGCCTCCCGTAGGAGT-3'

Probe 1660: 5'-CTGCTGCCTCCCGTAGGAGTTTGGGCCGTGTCTCAGTTCCAGTGT-3'

Probe 1661: 5'-TATTACCGCGGCTGCTGGCACGGAGTTAGCCG-3'

Probe 1739: 5'-GCGTGGACTACCGGGGTATCTAATCCTGTTTGCTCCCCACGCTTTCG-3'

Probe 1740: 5'-GGGTTGCGCTCGTTGCGGGACTTAACCCGACATCTCACGGCACGAGCT GACGACAGCCATGCAT-3'

Probe 1741: 5'-CTCACGGCACGAGCTGACGACAGCCATGCAT-3'

Probe 1742: 5'-GGGTTGCGCTCGTTGCGGGACTTAACCCGACAT-3'

Probe 1745: 5'-AGCTGACGACAACCATGCACCACCTGT-3'

Probe 1746: 5'TCATAAGGGGCATGATGATTTGACGTCAT-3'

Probe 1743: 5'-GTACAAGGCCCGGGAACGTATTCACCG-3'

Probe 1637: 5'-AAGGAGGTGATCCAGCC-3'

Probe 1639: 5'-ACGGTTACCTTGTTACGACTT-3'

Probe 1640: 5'-ACGGCTACCTTGTTACGACTT-3'

Probe 1641: 5'-ACGGATACCTTGTTACGACTT-3'

23S rRNA-targeted probes:

Probe 1730: 5'-CTTTTCTCCTTTCCCTCRCGGTACTGGTTCRCTATCGGTC'3

Probe 1731: 5'-CTTTTCGCCTTTCCCTCGCGGTACTGGTTCGCTATCGGTC'3

Probe 1658: 5'-TCTTTAAAGGGTGGCTGCTTCTAAGCCAACATCCTGGTTG-3'

Probe 1656: 5'-CTACCTGTGTCGGTTTGCGGTACGGGC-3'

Probe 1657: 5'-GGTATTCTCTACCTGACCACCTGTGTCGGTTTGGGGTACG-3'

Probe 1653: 5'-CCTTCTCCCGAAGTTACGGGGGCATTTTGCCTAGTTCCTT-3'

Probe 1654: 5'-CCTTCTCCCGAAGTTACGGGGTCATTTTGCCGAGTTCCTT-3'

Probe 1655: 5'-CCTTCTCCCGAAGTTACGGCACCATTTTGCCGAGTTCCTT-3'

Probe 1651: 5'-CTCCTCTTAACCTTCCAGCACCGGGCAGGC-3'

Probe 1652: 5'-TTCGATCAGGGGCTTCGCTTGCGCTGACCCCATCAATTAA-3'

Probe 1512: 5'-TTAGGACCGTTATAGTTACGGCCGCCGTTTACTGGGGCTT-3'

Probe 1256: 5'-GGTCGGAACTTACCCGACAAGGAATTTCGCTACCTTAG-3'

Probe 1398: 5'-GGTCGGTATTTAACCGACAAGGAATTTCGCTACCTTAG-3'

Probe 1511: 5'-CGTGCGGGTCGGAACTTACCCGACAAGGAATTTCGCTACC3'

Probe 1595: 5'-CGATATGAACTCTTGGGCGGTATCAGCCTGTTATCCCCGG-3'

Probe 1600: 5'-CAGCCCCAGGATGAGATGAGCCGACATCGAGGTGCCAAAC-3'

Probe 1601: 5'-CAGCCCCAGGATGTGATGAGCCGACATCGAGGTGCCAAAC-3'

Probe 1602: 5'-CAGCCCCAGGATGCGATGAGCCGACATCGAGGTGCCAAAC-3'

Probe 1598: 5'-CGTACCGCTTTAAATGGCGAACAGCCATACCCTTGGGACC-3'

Probe 1599: 5'-CGTGCCGCTTTAATGGGCGAACAGCCCAACCCTTGGGACC-3'

Probe 1596: 5'-GATAGGGACCGAACTGTCTCACGACGTTTTGAACCCAGCT-3'

Probe 1597: 5'-GATAGGGACCGAACTGTCTCACGACGTTCTGAACCCAGCT-3'

The specific behaviors of the aforementioned probes are dependent to a significant extent on the assay format in which they are employed. Conversely, the assay format will dictate certain of the optimal design features of particular probes. The "essence" of the probes of the invention is not to be construed as restricted to the specific string of nucleotides in the named probes. For example, the length of these particular oligonucleotides was optimized for use in the dot blot assay (and certain other anticipated assays) described below. It is well known to those skilled in the art that optimal probe length will be a function of the stringency of the hybridization conditions chosen and hence the length of the instant probes may be altered in accordance therevith. Also, in considering sets comprised of more than one probe, it is desirable that all probes behave in a compatible manner in any particular format in which they are employed. Thus, the exact length

of a particular probe will to a certain extent, reflect its specific intended use. Again, given the probes of the instant invention, these are familiar considerations to one of ordinary skill in the art.

The "essence" of the probes described herein resides in the discovery and utilization of the specific sequences described above and given in Table 1 and Table 2.

Hybridization Analysis of Probe Behavior:

The sequence comparisons which led to the discovery of the disclosed target sequences suggested that many of the probes should hybridize to a significant number of eubacteria. For the 16S rRNA analyses, some 350 sequences were considered in designing the probes; for the 23S rRNA analyses only about 30 eubacterial sequences were available. Since it is impossible to test every eubacterial strain, greater sequence variation might exist in other eubacterial strains not inspected by sequence analysis which might reduce or eliminate hybridization by the prospective probes to such untested eubacteria. As can be seen in Tables 3, 4 and 5, some probes of extremely broad inclusivity nevertheless fail to hybridize to certain bacteria. Therefore, carefully documenting the hybridization behavior to a large and representative number of eubacteria is an important element in documenting that such probes are capable of detecting all eubacteria or, failing that, for documenting which eubacteria are not detected. Such "failures" may not be clinically significant or alternatively, may be compensated for by appropriate inclusion of other probes of the instant inventions.

Equally as important as the inclusivity behavior of the probes, is their exclusivity behavior, i.e., their reactivity toward non-eubacteria. As mentioned, demonstrating a lack of hybridization to human and fungal rRNAs is of paramount importance in the types of clinical applications envisioned for such probes. Therefore, the

behavior of the probes toward representative eubacterial, human and fungal rRNAs was determined by hybridization analysis using a dot blot procedure.

Example 1: Dot-blot analysis of probe hybridization behavior.

Dot-blot analysis, in accordance with well known procedures, involves immobilizing a nucleic acid or a population of nucleic acids on a filter such as nitrocellulose, nylon, or other derivatized membranes which readily can be obtained commercially, specifically for this purpose. Either DNA or RNA can be easily immobilized on such a filter and subsequently can be probed or tested for hybridization under any of a variety of conditions (i.e., stringencies) with nucleotide sequences or probes of interest. Under stringent conditions, probes whose nucleotide sequences have greater complementarity to the target sequence will exhibit a higher level of hybridization than probes containing less complementarity. For most of the oligonucleotide probes described herein, hybridization to rRNA targets at 60°C for 14-16 hours (in a hybridization solution containing 0.9 M NaCl, 0.12 M Tris-HCl, pH 7.8, 6 mM EDTA, 0.1 M KPO4, 0.1% SDS, 0.1% pyrophosphate, 0. 002% ficoll, 0.02% BSA, and 0.002% polyvinylpyrrolidine), followed by standard post-hybridization washes to remove unbound and non-specifically hybridized probe (at 60°C in 0.03 M NaCl, 0. 004 M Tris-HCl, pH 7.8, 0.2 mM EDTA, and 0.1% SDS), would be sufficiently stringent to produce the levels of specificity demonstrated in Tables 3, 4 and 5. The exceptions to these conditions are probe 1738 (which was hybridized at 37°C), and probe 1746 (which was hybridized at 37°C and washed at 50°C).

Techniques also are available in which DNA or RNA present in crude (unpurified) cell lysates can be immobilized without first having to purify the nucleic acid in question (e.g. Maniatis, T., Fritsch, E. F. and Sambrook, J., 1982, Molecular Cloning:A Laboratory Manual).

The dot-blot hybridization data shown in Tables 3, 4 and 5 were generated by hybridization of the indicated probes to purified RNA preparations from the indicated eubacterial, fungal and human specimens. Bacterial and fungal RNAs were purified from pure cultures of the indicated organisms. Mouse RNA was purified from L cells (a tissue culture cell line). Wheat germ RNA was purified from a commercial preparation of that cereal product. Human blood and stool RNAs were purified from appropriate specimens obtained from normal, healthy individuals.

Purified RNA was used, rather than cell lysates for a number of simple technical reasons. The most important of these relate to proper interpretation of the relative signal arising from the hybridization of any particular probe to individual organisms. RNA content per cell is known to vary widely among different bacteria and varies even more between bacteria and eukaryotic cells. In addition, the specific metabolic status of cells at the time of harvest can have a profound influence on the amount and integrity of the RNA recovered. Some bacteria, for example, begin to degrade their RNA very rapidly upon reaching the stationary growth phase. The organisms represented in Tables 3, 4 and 5 comprise an extremely diverse collection in every respect. Represented are Gram positive and Gram negative bacteria, photosynthetic and chemosynthetic, heterotrophic and lithotrophic, and anaerobic and aerobic metabolisms. By using known, equivalent amounts of purified RNA in the individual "dots," relative levels of hybridization of each probe to each organism can be meaningfully compared without regard to the idiosyncracies of nucleic acid preparation from individual types of bacteria represented.

RNA was prepared by a variation on standard published methods which has been developed in our laboratory (W. Weisburg, unpublished). The method rapidly yields bulk high molecular weight RNA in a highly purified but relatively unfractionated form. Little or no DNA, or low molecular weight RNA species are found in RNA prepared in this fashion.

A large proportion of the RNA is 16S and 23S rRNA (18S and 28S rRNA in eukaryotes) as is true of the RNA in the intact cells. The method is rapid and convenient, but otherwise is not relevant to interpretation of the dot-blot results presented in Tables 3, 4 and 5. Most other currently accepted methods available in the literature which yield RNA of reasonable intactness will yield equivalent hybridization results.

For the hybridization experiments reported in Tables 3, 4 and 5, probes were end-labeled with radioactive 32-phosphorous , using standard procedures. Following hybridization and washing as described above, the hybridization filters were exposed to X-ray film and the intensity of the signal evaluated with respect to that of control RNA spots containing known amount of target RNA of known sequence.

A scale of hybridization intensity ranging from ++++ (hybridization signal equivalent to that of control spots) to + (barely detectable even after long exposure of the x-ray film) has been used to compare hybridization signals between organisms and probes. +++ signal indicates a very strong signal only slightly less intense than control spots. ++ indicates a clearly discernible hybridization signal, but one that is noticeably weaker than the control spots. Note that while more "quantitative" ways to record hybridization signal are available, they are much more cumbersome to employ and, in our experience, not really any more useful for probe evaluation than the method employed in Tables 3, 4 and 5. In fact, because of certain uncontrollable variables in spotting exactly equivalent amounts of target RNA (of equivalent intactness) from such disparate organisms, numerically more precise counting methods are only deceptively more quantitative. In our experience, an organism generating a ++ or greater signal to a particular probe is easily distinguished from one generating a "-" signal. This is true of a variety of assay formats that have been tested.

As is evident in Tables 3 and 4, 23S rRNA-targeted probes 1600, 1602, 1596, 1256 and 1512 and 16S rRNA-targeted probes, 1738, 1660, 1639, 1739, 1740, 1741 and 1743 hybridize most extensively among the eubacteria and are thus the most preferred. Other probes hybridize in a variety of patterns to subgroups of eubacteria and would be preferred for the detection of those subgroups or as components of more broadly inclusive probe sets. For example, probes 1599, 1656, 1744, 1745 and 1746 hybridize preferentially to Gram positive bacteria. Probes 1657, 1598 and 1595 hybridize preferentially to gram-negative bacteria, particularly to members of the so-called "purple bacterial" division (Figure 2 and Table 5).

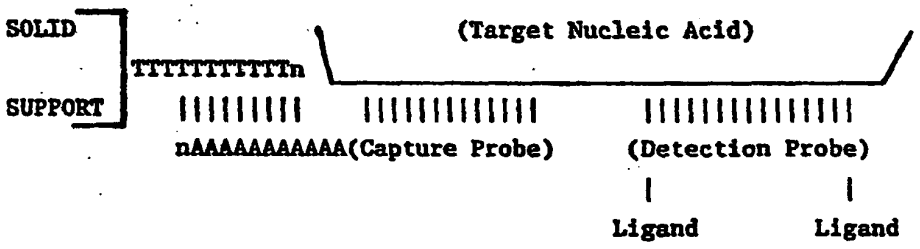
Other probes exhibit other useful patterns of hybridization as is evident upon inspection of the data in Tables 3, 4 and 5. These probes can be combined in a variety of ways to create probe sets which exhibit the combined hybridization properties of the component probes. An example of one such hybridization format is given below (Example 2).

Alternatively, the probes could be used in a variety of subtractive hybridization schemes in which specific rRNA molecules are removed from the pool present in a mixed population of organisms prior to or simultaneous with the target organism-specific probes (e.g. Collins, European Patent Application 87309308.2).

Example 2: Dual Probe, Sandwich Hybridization Assay

The probes of the present invention or derivatives thereof can be advantageously employed in a variety of other hybridization formats. One such format is a dual probe, sandwich-type hybridization assay such as that described, for example, in USSN 277,579; USSN 169,646, or USSN 233,683. In such a dual probe application, one probe (for example, probe 1602 or a derivative) would be ideally modified at its 3' terminus to contain a tract of about 20 - 200 deoxyadenosine (dA) residues. This would be used to "capture" the target rRNA (following

liquid hybridization) from the test sample onto a solid support (e.g., beads, plastic surface, filter, etc.) which had been suitably derivatized with poly-deoxythymidine (dT) for this purpose. A second probe (for example, probe 1596 or derivative) would then be advantageously used as the detection probe and would be suitably derivatized with some detectable ligand (e.g. 32-P, fluorescein, biotin, etc.). Detection of the presence of the target nucleic acid in a test sample then would be indicated by capture of the detection ligand onto the solid surface through the series of hybridization interactions:



This could occur only if the target nucleic acid is present in the test sample. In principle, the above scheme could be employed with multiple capture and detection probes (probe sets) for the purpose of, for example, improving inclusivity or enhancing sensitivity of the assay.

Example 3: PCR Amplification of 16S rRNAs.

The polymerase chain reaction (PCR) is a well known method for amplifying target nucleic acid by "copying" the nucleic acid sequences located between two target sequences (US 4,683,202). The PCR process could be useful in an assay for the diagnosis of, for example, a non-viral pathogen by amplifying the genes encoding the pathogen's rRNA or rRNA genes and subsequently detecting that product. Implementation of this diagnostic strategy requires the invention of primers capable of

amplifying the rRNA of the targeted organism(s). A second important application of such primers is in cloning amplified rRNA genes, and a third application is the direct sequencing of amplified rRNA genes.

Probes 1638, 1642, 1643, 1637, 1639, 1640 and 1641 may be ideally used as primers for enzymatically copying and/or amplifying eubacterial 16S rRNAs or the genes encoding them. Details of the PCR procedure vary slightly depending on whether the target nucleic acid is single or double stranded, and whether it is DNA or RNA. However, the principle is the same in either case. Briefly, the steps are as follows:

1) Double-stranded DNA is denatured,

2) Oligonucleotide primers complimentary to each of the sister DNA strands are annealed, and

3) deoxynucleotide triphosphate precursors are incorporated into newly synthesized sister DNA strands by extension of the primers from their 3' termini using DNA polymerase and/or reverse transcriptase.

Thus, a pair of oligonucleotide primers are required for the PCR reaction, one complementary to each strand within the target gene. They are positioned such that the newly synthesized product of one primer is also a target/template for the other primer. Thus the target nucleotide sequence located between the two primer annealing sites may be amplified many fold by repeating the steps listed above 20 to 30 times.

Probes 1638, 1642, 1643, 1637, 1639, 1640 and 1641 are suitable for use as primers for enzymatically copying and/or amplifying eubacterial 16S rRNAs or the genes encoding them. That is, as a set, they will anneal very broadly among eubacterial rRNAs and rRNA genes and so will amplify any eubacterial rRNA sequences present in a sample.

Probes 1637, 1639, 1640 and 1641 hybridize to the 16S rRNA (or rRNA-like strand of the ribosomal RNA gene) near its 3′ end (Table 1). The template strand is read in the 3′ to 5′ direction producing an rRNA-complementary strand with the primer itself incorporated at its 5′ terminus.

Probes 1638, 1642, and 1643 hybridize near the 5′ end of the rRNA-complementary strand of the rRNA gene or to such a complement produced as described immediately above.

Individually, the above-described 16S rRNA amplification primers have approximately the following specificities:

5′ primers:

Probe 1638: most eubacteria

Probe 1642: enterics and relatives

Probe 1643: Borrelia spirochetes

3′ primers:

Probe 1637: most eubacteria

Probe 1639: enterics, Deinococcus, Campylobacter

Probe 1640: most eubacteria

Probe 1641: fusobacteria, some Bacillus species

In test samples where the target bacterium is known, specific primers can be used. Where the target organism is not specifically known (for example, any eubacterium) all of the above mentioned primers can be used as a set.

The above described primers have been designed to amplify nearly the entire 16S rRNA sequence. Any of the other probes of the present invention or derivatives thereof can be used to amplify sub-segments of the 16S and 23S rRNAs or genes in a fashion similar to that just described.

Any such primers can be modified in a great number of ways to, for example, incorporate RNA polymerase promoters, cloning sites, etc. into the amplified transcripts.

While the description of the invention has been made with reference to detecting rRNA, it will be readily understood that the probes described herein and probes complementary to those described herein also will be useful for the detection of the genes (DNA) which specify the rRNA and, accordingly, such probes are to be deemed equivalents to the described probes and encompassed within the spirit and scope to the present invention and the appended claims.

TABLE 1: 16S rRNA-TARGETED PROBES AND TARGET SEQUENCES

```
E. coli#s              8                                  38
                       |                                  |
CONS-90%               AGAGUUUGAUC UGGCUCAG   GAACGCUGGCG
E. coli      5'-AAAUUGAAGAGUUUGAUCAUGGCUCAGAUUGAACGCUGGCG
Probe 1738           3'-TCTCAAACTAGGACCGAGTC-5'
Probe 1744             3'-TCAAACTAGGACCGAGTCCTGCTTGCGAC-5'
Probe 1638           5'-AGAGTTTGATCCTGGCTCAG-3'
Probe 1642           5'-AGAGTTTGATCATGGCTCAG-3'
Probe 1643           5'-AGAGTTTGATCCTGGCTTAG-3'


E.  coli#s     313                                          357
               |                                            |
CONS-90%       G CACA UGG ACUGAGACACGG CCA ACUCCUACGGGAGGCAGCAGU
E. coli        GCCACACUGGAACUGAGACACGGUCCAGACUCCUACGGGAGGCAGCAGUGG
Probe 1660     3'-TGTGACCTTGACTCTGTGCCGGGTTTGAGGATGCCCTCCGTCGTC-5'
Probe 1659                                 3'-TGAGGATGCCCTCCGTCGTC-5'


E. coli#s      504                                  535
               |                                    |
CONS-90%       C  CGGCUAACU  GUGCCAGCAGCCGCGGUAAUAC
E. coli        CACCGGCUAACUCCGUGCCAGCAGCCGCGGUAAUACGG
Probe 1661     3'-GCCGATTGAGGCACGGTCGTCGGCGCCATTAT-5'


E. coli#s      764                                                  810
               |                                                    |
CONS-90%       G  CGAAAGCGUGGGGAGC AACAGGAUUAGAUACCCUGGUAGUCCACGC  U
E. coli        GUGCGAAAGCGUGGGGAGCAAACAGGAUUAGAUACCCUGGUAGUCCACGCCGU
Probe 1739     3'-GCTTTCGCACCCCTCGTTTGTCCTAATCTATGGGGCCATCAGGTGCG-5'
```

TABLE 1 (cont'd): 16S rRNA-TARGETED PROBES AND TARGET SEQUENCES

```
E. coli#s    1044                                                          1114
             |                                                             |
CONS-90%      ACAGGUG UGCAUGG UGUCGUCAGCUCGUG CGUGAG UGUUGGGUUAAGUCCCGCAACGAGCGCAACCC
E. coli     GAGACAGGUGCUGCAUGGCUGUCGUCAGCUCGUGUUGUGAAAUGUUGGGUUAAGUCCCGCAACGAGCGCAACCCUUA
Probe 1745  3'-TGTCCACCACGTACCAACAGCAGTCGA-5'
Probe 1740        3'-TACGTACCGACAGCAGTCGAGCACGGCACTCTACAGCCCAATTCAGGGCGTTGCTCGCGTTGGG-5'
Probe 1741        3'-TACGTACCGACAGCAGTCGAGCACGGCACTC-5'
Probe 1742                                          3'-TACAGCCCAATTCAGGGCGTTGCTCGCGTTGGG-5'

E. coli#s    1188                          1216
             |                             |
CONS-90%      GGA GACGUCAA UC UCAUG CCCUUA G
E. coli     GGGAUGACGUCAAGUCAUCAUGGCCCUUACGACCA
Probe 1746  3'-TACTGCAGTTTAGTAGTACGGGGAATACT-5'

E. coli#s    1369                    1395
             |                       |
CONS-90%      CGGUGAAUACGUUC CGGG CUUGUACACA
E. coli     CCACGGUGAAUACGUUCCCGGGCCUUGUACACA
Probe 1743  3'-GCCACTTATGCAAGGGCCCGGAACATG-5'

E. coli#s    1492                                                    1541
             |                                                       |
CONS-90%      AAGUCGUAACAAGGUA CC UA   GAA  UG GG UGGAU ACCUCCUUU
E. coli     GUGAAGUCGUAACAAGGUAACCGUAGGGGAACCUGCGGUUGGAUCACCUCCUUA-3'
Probe 1637                                          3'-CCGACCTAGTGGAGGAA-5'
Probe 1639  3'-TTCAGCATTGTTCCATTGGCA-5'
Probe 1640  3'-TTCAGCATTGTTCCATCGGCA-5'
Probe 1641  3'-TTCAGCATTGTTCCATAGGCA-5'
```

TABLE 2: 23S rRNA-TARGETED PROBES AND TARGET SEQUENCES

```
E. coli #s    442                                          481
              |                                            |
CONS-90%       GACCGAUAG G AC AGUACCGUGAGGGAAAGG GAAAAG AC
E.coli 23S    ACUGACCGAUAGUGAACCAGUACCGUGAGGGAAAGGCGAAAAGAAC
Probe 1730    3'-CTGGCTATCRCTTGGTCATGGCRCTCCCTTTCCRCTTTTC-5'
Probe 1731    3'-CTGGCTATCGCTTGGTCATGGCGCTCCCTTTCCGCTTTTC-5'

E. coli #s    1049                                         1088
              |                                            |
CONS-90%      A ACA C AGGA GUUGGCUUAGAAGCAGCCA C UU AAAGA  G
E.coli 23S    AGACAGCCAGGAUGUUGGCUUAGAAGCAGCCAUCAUUUAAAGAAAG
Probe 1658    3'-GTTGGTCCTACAACCGAATCTTCGTCGGTGGGAAATTTCT-5'

E. coli #s    1597                                            1639
              |                                               |
CONS-90%         CGUACC  AAACCGACACAGGU G    G   A  A  C  AG
E.coli 23S    UCAAAUCGUACCCCAAACCGACACAGGUGGUCAGGUAGAGAAUACCAAG
Probe 1656    3'-CGGGCATGGCGTTTGGCTGTGTCCATC-5'
Probe 1657       3'-GCATGGGGTTTGGCTGTGTCCACCAGTCCATCTCTTATGG-5'

E. coli #s    1664                                         1703
              |                                            |
CONS-90%       AAGGAACU  GCAAA U    CCGUAACUUCGG A AAGG
E.coli 23S    GUGAAGGAACUAGGCAAAAUGGUGCCGUAACUUCGGGAGAAGGCAC
Probe 1653    3'-TTCCTTGATCCGTTTTACGGGGGCATTGAAGCCCTCTTCC-5'
Probe 1654    3'-TTCCTTGAGCCGTTTTACTGGGGCATTGAAGCCCTCTTCC-5'
Probe 1655    3'-TTCCTTGAGCCGTTTTACCACGGCATTGAAGCCCTCTTCC-5'

E. coli #s    1831                              1860
              |                                 |
CONS-90%      GAC CCUGCCC GUGC GGAAGGUUAA  G
E.coli 23S    GACGCCUGCCCGGUGCCGGAAGGUUAAUUGAUGGGG
Probe 1651    3'-CGGACGGGCCACGACCTTCCAATTCTCCTC-5'

E. coli #s    1851                                         1890
              |                                            |
CONS-90%      AGGUUAA  G    U        G  AAG      A  GAAGCC
E.coli 23S    AGGUUAAUUGAUGGGGUUAGCGCAAGCGAAGCUCUUGAUCGAAGCC
Probe 1652    3'-AATTAACTACCCCAGTCGCGTTCGCTTCGGGGACTAGCTT-5'
```

TABLE 2 (cont'd): 23S rRNA-TARGETED PROBES AND TARGET SEQUENCES

```
E. coli #s   1889                                                1928
CONS-90%      GAAGCCCC GU AACGGCGGCCGUAACUAUAACGGUCCUAAGGU
E.coli 23S   UCGAAGCCCCGGUAAACGGCGGCCGUAACUAUAACGGUCCUAAGGU
Probe 1512   3'-TTCGGGGTCATTTGCCGCCGGCATTGATATTGCCAGGATT-5'

E. coli #s   1925                                                1968
CONS-90%     GUCCUAAGGUAGCGAAAUUCCUUGUCGGGUAAGUUCCGACC GCACGAA
E.coli 23S   GUCCUAAGGUAGCGAAAUUCCUUGUCGGGUAAGUUCCGACCUGCACGAAU
Probe 1256   3'-GATTCCATCGCTTTAAGGAACAGCCCATTCAAGGCTGG-5'
Probe 1511      3'-CCATCGCTTTAAGGAACAGCCCATTCAAGGCTGGGCGTGC-5'
Probe 1398   3'-GATTCCATCGCTTTAAGGAACAGCCAATTTATGGCTGG-5'

E. coli #s   2442                                                2481
CONS-90%     AC C GGGGAUAACAGGCU AU  C  CC AG GU CA AUCG CG
E.coli 23S   ACUCCGGGGAUAACAGGCUGAUACCGCCCAAGAGUUCAUAUCGACG
Probe 1595   3'-GGCCCCTATTGTCCGACTATGGCGGGTTCTCAAGTATAGC-5'

E. coli #s   2490                                                2529
CONS-90%       GUUUGGCACCUCGAUGUCGGCUC UC CAUCCUGGGGCUG AG
E.coli 23S   GGUGUUUGGCACCUCGAUGUCGGCUCAUCACAUCCUGGGGCUGAAG
Probe 1600   3'-CAAACCGTGGAGCTACAGCCGAGTAGAGTAGGACCCCGAC-5'
Probe 1601   3'-CAAACCGTGGAGCTACAGCCGAGTAGTGTAGGACCCCGAC-5'
Probe 1602   3'-CAAACCGTGGAGCTACAGCCGAGTAGCGTAGGACCCCGAC-5'

E. coli #s   2535                                                2574
CONS-90%     G  GGUCCCAAGGGU  GGCUGUUCGCC  UUAAAG GG ACG GA
E.coli 23S   GUAGGUCCCAAGGGUAUGGCUGUUCGCCAUUUAAAGUGGUACGCGA
Probe 1598   3'-CCAGGGTTCCCATACCGACAAGCGGTAAATTTCGCCATGC-5'
Probe 1599   3'-CCAGGGTTCCCAACCCGACAAGCGGGTAATTTCGCCGTGC-5'

E. coli #s   2577                                                2616
CONS-90%     G GAGCUGGGUU A AACGUCGUGAGACAGUU GGUC CUAUC
E.coli 23S   GCGAGCUGGGUUUAGAACGUCGUGAGACAGUUCGGUCCCUAUCUGC
Probe 1596   3'-TCGACCCAAGTTTTGCAGCACTCTGTCAAGCCAGGGATAG-5'
Prob  1597   3'-TCGACCCAAGTCTTGCAGCACTCTGTCAAGCCAGGGATAG-5'
```

TABLE 3: DOT BLOT HYBRIDIZATION of 16S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1738	1739	1659	1660	1661	1740	1741	1742	1743
Acinetobacter calcoaceticus	GT0002	Purple	++++	++++	++++	++++	++++	++++	++++	++++	++++
Aeromonas sobria	GT0007	gamma	++++	++++	++++	++++	++++	++++	++++	++++	++++
Alteromonas putrefaciens	GT1945	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Citrobacter amalonaticus	GT0690	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Citrobacter diversus	GT0030	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Citrobacter freundii	GT0687	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Edwardsiella tarda	GT0569	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Enterobacter agglomerans	GT0683	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Enterobacter cloacae	GT0686	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Enterobacter sakazakii	GT0062	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Escherichia coli	GT1665	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Escherichia coli	GT1592	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Escherichia coli	GT1659	"	+++	++++	++++	++++	++++	++++	++++	++++	++++
Haemophilus influenza	GT0244	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Haemophilus ducreyi	GT0243	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Hafnia alvei	GT0241	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
M rgenella morganii	GT0303	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Klebsiella pneumoniae	GT1500	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Pr t us mirabilis	GT1496	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Providencia alcalifaciens	GT0371	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Pseudomonas aeruginosa	GT1909	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Salm nella arizona	GT0799	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Salmonella typhimurium	GT0389	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Serratia marcescens	GT0392	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Shigella flexneri	GT0798	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Vibri parahaemolyticus	GT0568	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Xanthomonas maltophilia	GT0417	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Yersinia enterocolitica	GT0419	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Alcaligenes faecalis	GT0610	Purple	++++	++++	++++	++++	++++	++++	++++	++++	++++
Branhamella catarrhalis	GT0014	beta	+++	++++	++++	++++	++++	++++	++++	++++	++++
Chromobacterium violaceum	GT2022	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Kingella indologenes	0246	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Moraxella osloensis	GT0301	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
M rax lla phenylpyruvica	GT0302	"	+++	++++	++++	++++	++++	++++	++++	++++	++++

TABLE 3 (cont'd): DOT BLOT HYBRIDIZATION of 16S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1738	1739	1659	1660	1661	1740	1741	1742	1743
Borrelia burgdorferi		Spiro	++++	++++	++++	++++	++++	++++	++++	++++	++++
Borrelia turicatae		"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Leptospira interrogans-pomona		"	++++	+++	++++	++++	++++	++++	++++	++++	++
Leptospira biflexa (Patoc-Patoc)		"	++++	++	++++	++++	++++	++++	++++	++++	+
Leptospira biflexa (CDC)		"	++++	+++	++++	++++	++++	++++	++++	++++	++
Spirochaeta aurantia		"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Bacteroides fragilis	25285	Bact	++++	+++	++++	++++	++++	++++	++++	-	++++
Bacteroides fragilis	29771	"	++++	+++	++++	++++	++++	++++	++++	-	++++
Bacteroides thetaiotaomicron	0572	"	++++	++	++++	++++	++++	++++	++++	-	++++
Bacteroides melaninogenicus	0011	"	++++	++	++++	++++	++++	++++	++++	-	++++
Flavobacterium meningosepticum	0237	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Chlamydia psittaci		Chlam	-	++++	-	+++	++++	++++	++++	++++	++++
Chlamydia trachomatis		"	-	++++	-	+++	++++	++++	++++	++++	++++
Chlorobium limicola		Misc	++++	++++	++++	++++	++++	++++	++++	++++	+
Chlor flexus aurantiacus	Y400	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Deinoc ccus radiodurans	2608	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Planct myces maris	2577	"	++++	++++	-	++++	++++	++++	++++	-	-
Normal Stool RNA			++++	++++	++++	++++	++++	++++	++++	++++	++++
Mouse L-Cell			-	+	-	-	++	-	-	-	-
Wheat Germ			-	-	-	-	++	-	-	-	-
N rmal Human Blood			-	-	-	-	++	-	-	-	-
Candida lusitaniae	403-87		-	-	-	-	++++	-	-	-	-
Candida parapsilosis	882-88		-	-	-	-	++++	-	-	-	-
Candida tropicalis	224-87		-	-	-	-	++++	-	-	-	-
Candida albicans	1008-88		-	-	-	-	++++	-	-	-	-
Candida albicans	223-87		-	-	-	-	++++	-	-	-	-
Candida albicans	819-88		-	-	-	-	++++	-	-	-	-

* Inclusivity and Exclusivity data was determined after overnight exposures.
** Each organism is represented by 100ng of CsTFA purified RNA.
*** Probe 1738 - hybridizations and washes were carried out at 37 C. ++++ = positive c ntrol level of hybridization, + = barely detectable and - = zero, ND = not done.

TABLE 3 (cont'd): DOT BLOT HYBRIDIZATION of 16S rRNA-TARGETED PROBES

			PROBE HYBRIDIZATION								
G nus species	strain	div	1738	1739	1659	1660	1661	1740	1741	1742	1743
Myc plasma pneumoniae	ATCC15531	"	++++	++++	++++	++++	-	++++	++++	++++	-
Myc plasma putrefaciens	ATCC15718	"	++++	++++	++++	++++	++++	++++	++++	++++	-
P ptostreptococcus productus	ATCC27340	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Planococcus citreus	ATCC14404	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Staphlyococcus aureus	GT0399	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Staphylococcus aureus	GT1711	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Staphylococcus epidermidis	GT0401	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Staphylococcus haemolyticus	ATCC29970	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Streptococcus agalactiae	GT0405	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Streptococcus bovis	GT0668	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Streptococcus faecalis	GT0406	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Streptococcus morbillorum	GT2194	"	++	++++	++++	++++	++++	++++	++++	++++	++++
Streptococcus mutans	GT0412	"	+++	++++	++++	++++	++++	++++	++++	++++	++++
Str ptococcus pneumoniae	GT0408	"	+++	++++	++++	++++	++++	++++	++++	++++	++++
Streptococcus salivarius	GT0410	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Streptococcus sanguis	GT0411	"	++++	++++	++++	++++	++++	++++	++++	++++	ND
Bifidobacterium dentium	GT0012	hiG+C	-	++++	++++	++++	++++	++++	++++	++++	++++
Corynebacterium genitalium	GT0045	Gm +	++++	++++	++++	++++	++++	++++	++++	++++	++++
C rynebacterium glutamicum	GT2120	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Corynebacter. pseudodiphtheriticum	GT2119	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Corynebacterium pseudotuberculosis	GT2122	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Corynebacterium pyogenes	GT2121	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
C rynebacterium xerosis	GT0046	"	++	+++	++++	++++	++++	++++	++++	++++	++++
Mycobacterium bovis	BCG	"	++	++++	++++	++++	++++	++++	++++	++++	++++
Myc bacterium kansasii		"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Nocardia asteroides	GT2191	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Rhodococcus rhodochrous		Misc	++++	++++	++++	++++	++++	++++	++++	++++	++++
Aerococcus viridans	GT2116	Gm +	++++	++++	++++	++++	++++	++++	++++	++++	-
Fusobacterium necrophorum	GT0238	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Fusobacterium prausnitzii	ATCC27768	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Gemella haemolysans	GT2118	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
H liobacillus mobilis		"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Phormidium ectocarpi		Cyano	++++	++	++++	++++	++++	++++	++++	++++	++++
Plectonema boryanum		"	++++	++	++++	++++	++++	++++	++++	++++	++++

TABLE 3 (cont'd): DOT BLOT HYBRIDIZATION of 16S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1738	1739	1659	1660	1661	1740	1741	1742	1743
N isseria gonorrhoeae	GT0315	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Neisseria meningitidis	GT0349	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Pseudomonas acidovorans	GT0376	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Ps udomonas cepacia	GT2015	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Rhodocyclus gelatinosa	ATCC17013	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Vitreoscilla stercoraria		"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Achromobacter xerosis	GT0810	Purple	++++	++++	++++	++++	++++	++++	++++	++++	++++
Acidiphilium cryptum	ATCC33463	alpha	++++	++++	++++	++++	++++	++++	++++	++++	++++
Agr bacterium tumefaciens	GT2021	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Bruc lla abortus	ATCC23448	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Flavobacterium capsulatum	GT2025	"	++++	++++	++++	++++	++++	++++	++++	++++	+
Myc plana bullata	GT2023	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Pseudomonas diminuta	GT2020	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Rhodobacter sphaeroides	ATCC17023	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Rhodospirillum rubrum	ATCC25903	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Thiobacillus versutus	ATCC25364	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Desulfovibrio desulfuricans	ATCC 7757	delta	++++	++++	++++	++++	++++	++++	++++	++++	++++
Cardi bacterium hominis	GT2095	Gm -	++++	++++	++++	++++	++++	++++	++++	++++	++++
Francisella tularensis	GT2172	Gm -	++++	++++	++++	++++	++++	++++	-	++++	++++
Campylobacter jejuni	GT0022	Campy	++++	++++	++++	++++	++++	++++	++++	++++	++++
Campylobacter pylori	GT0026	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Campylobacter sputorum	GT0027	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Bacillus brevis	GT0803	lowG+C	++++	++++	++++	++++	++++	++++	++++	++++	++++
Bacillus subtilis	GT0804	Gm +	++++	++++	++++	++++	++++	++++	++++	++++	++++
Cl stridium clostridioforme	ATCC25537	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Clostridium sordellii	GT0567	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Clostridium sporogenes	ATCC 3587	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Clostridium histolyticum	ATCC19401	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Clostridium perfringens	ATCC13124	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Clostridium ramosum	ATCC25582	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Kurthia zopfii	ATCC33403	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Lactobacillus acidophilus	GT0256	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Lactobacillus plantarum	GT0258	"	++++	++++	++++	++++	++++	++++	++++	++++	++++
Listeria monocytogenes	IG3299	"	++++	++++	++++	++++	++++	++++	++++	++++	++++

TABLE 4: DOT BLOT HYBRIDIZATION OF 23S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1730	1731	1658	1653	1654	1655	1651
Acinetobacter calcoaceticus	GT0002	Purple	++++	+++	++++	++++	++++	++++	+++
Aeromonas sobria	GT0007	gamma	++++	++++	++++	+++	++++	++++	-
Alteromonas putrefaciens	GT1945	"	++++	+++	++++	+++	++++	++++	++
Citrobacter amalonaticus	GT0690	"	++++	+++	++++	+++	++++	++++	+++
Citrobacter diversus	GT0030	"	++++	+++	++	++++	++++	++++	++
Citrobacter freundii	GT0687	"	++++	++++	++++	+++	++++	++++	++
Edwardsiella tarda	GT0569	"	++++	++++	++++	++++	++++	++++	++++
Enterobacter agglomerans	GT0683	"	+++	+++	++++	++++	++++	++++	++
Enterobacter cloacae	GT0686	"	++++	++++	++++	++++	++++	++++	+++
Enterobacter sakazakii	GT0062	"	+++	++	++++	++++	++++	++++	++
Escherichia coli	GT1665	"	++++	+++	++++	++++	++++	++++	+++
Escherichia coli	GT1592	"	++++	++++	++++	++++	++++	++++	++++
Escherichia coli	GT1659	"	++	++	++	++++	+++	-	++++
Haemophilus influenza	GT0244	"	+++	+	++	++	++	-	++++
Haemophilus influenza	ATCC33391	"	ND	ND	ND	ND	ND	ND	ND
Haemophilus ducreyi	GT0243	"	++++	++++	++++	++++	++++	++++	++++
Hafnia alvei	GT0241	"	++++	++++	++++	++++	++++	++++	++
Morganella morganii	GT0303	"	++++	++++	++++	++++	++++	++++	++
Klebsiella pneumoniae	GT1500	"	++++	++++	++++	++++	++++	++++	+++
Proteus mirabilis	GT1496	"	++++	++++	++++	++++	++++	++++	++++
Providencia alcalifaciens	GT0371	"	++++	++++	++++	++++	++++	++++	++++
Pseudomonas aeruginosa	GT1909	"	++++	++++	++	++++	++++	++++	+++
Salmonella arizona	GT0799	"	++++	+++	++++	++++	+++	++++	+++
Salmonella typhimurium	GT0389	"	+++	+++	++++	++++	+++	++++	+++
Serratia marcescens	GT0392	"	++++	++++	++++	++++	+++	++++	++++
Shigella flexneri	GT0798	"	++++	++++	++++	+++	+++	++++	++++
Vibrio parahaemolyticus	GT0568	"	++++	++++	++++	+++	+++	++++	++
Xanthomonas maltophilia	GT0417	"	++++	++++	++++	+++	+++	-	+++
Yersinia enterocolitica	GT0419	"	++++	++++	++++	++++	+++	++++	+++
Alcaligines faecalis	GT0610	Purple	+++	+++	+	-	+++	++++	++
Branhamella catarrhalis	GT0014	beta	+++	+++	++++	++++	+++	++++	++++
Chromobacterium violaceum	GT2022	"	++++	++++	++++	-	+++	++++	+++
Kingella indologenes	0246	"	++++	+++	+++	++	++	++++	+
Moraxella osloensis	GT0301	"	++++	++++	++++	++++	+++	++++	++

TABLE 4 (cont'd): DOT BLOT HYBRIDIZATION OF 23S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1730	1731	1658	1653	1654	1655	1651
Morexella phenylpyruvica	GT0302	"	+++	+++	+	++++	+++	++++	++++
Neisseria gonorrhoeae	GT0315	"	+++	+++	++++	-	++++	++++	+
Neisseria meningitidis	GT0349	"	++++	++++	++++	-	+++	++++	++++
Pseudomonas acidovorans	GT0376	"	++++	++++	++++	-	+++	++++	++++
Pseudomonas cepacia	GT2015	"	++++	+++	+++	-	-	++	-
Rhodocyclus gelatinosa	ATCC17013	"	+++	+++	+++	-	++	-	++
Vitreoscilla stercoraria		"	++++	++++	+++	-	+++	+++	+++
Achromobacter xerosis	GT0810	Purple	+++	+++	+++	-	-	++	+++
Acidiphilium cryptum	ATCC33463	alpha	+	-	++	-	-	-	+++
Agrobacterium tumefaciens	GT2021	"	++	++	++++	-	-	-	+++
Brucella abortus	ATCC23448	"	++++	++++	++++	-	-	-	++++
Flavobacterium capsulatm	GT2025	"	+++	+++	++++	-	-	-	+++
Mycoplana bullata	GT2023	"	++++	+++	+	-	-	-	-
Pseudomonas diminuta	GT2020	"	+++	+++	+	-	-	-	-
Rhodobacter sphaeroides	ATCC17023	"	++++	++++	++++	-	-	-	++++
Rhodospirillum rubrum	ATCC25903	"	++++	++++	++++	++++	++++	-	++++
Thiobacillus versutus	ATCC25364	"	++++	++++	+++	-	-	-	+++
Desulfovibrio desulfuricans	ATCC 7757	delta	+++	+	++	+	+++	-	+++
Cardiobacterium hominis	GT2095	Gm -	+++	+++	-	-	+++	-	+
Francisella tularensis	GT2172	Gm -	++++	++++	++++	-	-	-	++
Campylobacter jejuni	GT0022	Campy	+++	+	++++	-	-	-	-
Campylobacter pylori	GT0026	"	++	++	++++	-	-	-	+++
Campylobacter sputorum	GT0027	"	+++	++	++++	-	-	-	-
Bacillus brevis	GT0803	lowG+C	+++	+++	++++	++++	++++	++++	++++
Bacillus subtilis	GT0804	Gm +	+++	+++	++++	++++	++++	++++	++++
Clostridium clostridioforme	ATCC25537	"	-	-	+	++++	++++	++++	++++
Clostridium sordellii	GT0567	"	++++	++++	++++	++++	++++	++++	+++
Clostridium sporogenes	ATCC 3587	"	+++	+++	++++	++++	++++	++++	++++
Clostridium histolyticum	ATCC19401	"	++++	++	+++	+++	++++	++	+++
Clostridium perfringens	ATCC13124	"	++++	+++	+++	-	++++	-	++++
Clostridium ramosum	ATCC25582	"	++++	+++	-	-	-	-	++++
Kurthia zopfii	ATCC33403	"	++++	++++	+++	++++	++++	+++	+++
Lactobacillus acidophilus	GT0256	"	+++	+++	-	+	++++	-	++++
Lactobacillus plantarum	GT0258	"	++++	+++	+++	++++	++++	+++	+++

TABLE 4 (cont'd): DOT BLOT HYBRIDIZATION OF 23S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1730	1731	1658	1653	1654	1655	1651
Listeria monocytogenes	IG3299	"	++++	+++	++++	++++	++++	+++	+++
Mycoplasma pneumoniae	ATCC15531	"	+++	++	+++	-	-	-	-
Mycoplasma putrefaciens	ATCC15718	"	+++	++	++	-	-	-	-
Peptostreptococcus productus	ATCC27340	"	-	-	++	++++	++++	++++	++++
Planococcus citreus	ATCC14404	"	+++	+++	++++	++++	++++	+++	+++
Staphylococcus aureus	GT0399	"	++++	++++	++++	++++	++++	+++	++++
Staphylococcus aureus	GT1711	"	++++	++++	++++	++++	++++	+++	+++
Staphylococcus epidermidis	GT0401	"	++++	++++	++++	+++	++++	+++	++++
Staphylococcus haemolyticus	ATCC29970	"	++++	++++	++++	++++	++++	+++	++++
Streptococcus agalactiae	GT0405	"	+++	+++	-	++++	++++	+++	++++
Streptococcus bovis	GT0668	"	++++	+++	-	+++	++++	+++	++++
Streptococcus faecalis	GT0406	"	++++	+++	+++	++++	++++	+++	+++
Streptococcus morbillorum	GT2194	"	+++	++	+++	++++	++++	+++	+++
Streptococcus mutans	GT0412	"	+++	++	-	++++	++++	+++	+++
Streptococcus pneumoniae	GT0408	"	++++	+++	-	+++	++++	+++	++++
Streptococcus salivarius	GT0410	"	+++	++	-	++++	++++	+++	++++
Streptococcus sanguis	GT0411	"	+++	+++	-	++++	++++	+++	++++
Bifidobacterium dentium	GT0012	hiG+C	+++	+++	-	-	-	-	++++
Corynebacterium genitalium	GT0045	Gm +	+++	+++	+++	++++	++++	++	++++
Crynebacterium glutamicum	GT2120	"	++++	+++	+++	++++	++++	++	++++
Corynebacterium pseudodiphtheriticum	GT2119	"	++++	++++	+++	++++	++++	++++	++++
Corynebacterium pseudotuberculosis	GT2122	"	++++	+++	-	++	++++	++	++++
Corynebacterium pyogenes	GT2121	"	+	-	++	++++	++++	+++	+++
Corynebacterium xerosis	GT0046	"	-	-	+	++++	++++	++	+++
Mycobacterium bovis	BCG	"	-	-	++	++++	++++	++	+++
Mycobacterium kansasii		"	+	-	+++	++++	++++	+++	++++
Nocardia asteroides	GT2191	"	++++	++++	+++	-	-	-	++++
Rhodococcus rhodochrous		"	+++	+++	+++	++++	+++	++	++++
Aerococcus viridans	GT2116	Misc	++++	++++	+++	+++	+++	++	++++
Fusobacterium necrophorum	GT0238	Gm +	++++	++++	-	+++	+++	+	-
Fusobacterium prausnitzii	ATCC27768	"	+++	-	++	++	+++	-	++++
Gemella haemolysans	GT2118	"	++++	++++	++++	++	++++	++++	++++
Heliobacillus mobilis		"	+++	++	++++	+++	++++	++++	++++
Phormidium ectocarpi		Cyano	+	++	-	+++	++++	++++	-

TABLE 4 (cont'd): DOT BLOT HYBRIDIZATION OF 23S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1730	1731	1658	1653	1654	1655	1651
Plectonema boryanum		"	++	++	-	++	++++	+++	-
Borrelia burgdorferi		Spiro	+++	++	++	-	-	-	+++
Borrelia turicatae		"	++++	+++	++++	-	-	-	+++
Leptospira interrogans-pomona		"	+++	++	++++	-	-	-	++
Leptospira biflexa (Patoc-Patoc)		"	+++	++	++++	-	-	-	++++
Leptospira biflexa (CDC)		"	+++	++	++++	-	-	-	++++
Spirochaeta aurantia		"	++++	++	++++	-	-	-	++++
Bacteroides fragilis	25285	Bact	++	++	+	-	-	-	++++
Bacteroides fragilis	29771	"	++	++	+	-	-	-	++++
Bacteroides thetaiotaomicron	0572	"	+	+	+	-	-	-	++++
Bacteroides melaninogenicus	0011	"	-	-	+	++	++	-	++++
Flavobacterium meningosepticum	0237	"	+	-	+	-	-	-	+++
Chlamydia psittaci		Chlam	-	-	-	-	-	-	-
Chlamydia trachomatis	LGV	"	+++	+++	-	-	-	-	-
Chlorobium limicola		Misc.	++++	+++	+	++++	++++	+++	+++
Chloroflexus aurantiacus	Y400	"	+	-	++	-	++	-	+
Deinococcus radiodurans	2608	"	++++	+++	+++	-	-	-	+
Planctomyces maris	2577	"	-	-	+++	-	-	-	-
Normal Stool RNA			+++	++	+++	++	+++	++	+++
Mouse L-Cell			-	-	-	-	-	-	-
Wheat Germ			+	++	-	-	-	-	-
Normal Human Blood			-	-	-	-	-	-	-
Candida lusitaniae	403-87		-	-	-	-	-	-	-
Candida parapsilosis	882-88		-	-	-	-	-	-	-
Candida tropicalis	224-87		-	-	-	-	-	-	-
Candida albicans	1008-88		-	-	-	-	-	-	-
Candida albicans	223-87		-	-	-	-	-	-	-
Candida albicans	819-88		-	-	-	-	-	-	-

* Inclusivity and Exclusivity data was determined after overnight exposures.
** Each organism is represented by 100ng of CsTFA purified RNA. ++++ = positive level of hybridization, + = barely detectable and - = zero, ND - not done.

TABLE 4 (cont'd): DOT BLOT HYBRIDIZATION OF 23S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1512	1256	1398	1600	1601	1602	1596	1597
Acinetobacter calcoaceticus	GT0002	Purple	++++	++++	+	++++	++++	++++	++++	++
Aeromonas sobria	GT0007	gamma	++++	++++	++	++++	++++	++++	++++	++
Alteromonas putrefaciens	GT1945	"	++++	++++	++	++++	++++	++++	++++	+++
Citrobacter amalonaticus	GT0690	"	++++	+++	+	++++	+++	++++	+++	+++
Citrobacter diversus	GT0030	"	++++	++++	+	++++	+++	++++	+++	+++
Citrobacter freundii	GT0687	"	++++	++++	+	++++	+++	++++	+++	++++
Edwardsiella tarda	GT0569	"	++++	++++	+	++++	++++	++++	+++	+++
Enterobacter agglomerans	GT0683	"	++++	++++	+	+++	+++	++++	+++	++
Enterobacter cloacae	GT0686	"	++++	++++	+	++++	+++	++++	+++	++
Enterobacter sakazakii	GT0062	"	++++	++++	++	+++	+++	++++	+++	++
Escherichia coli	GT1665	"	++++	++++	+	+++	+++	++++	+++	++++
Escherichia coli	GT1592	"	++++	++++	+	++++	++++	++++	++++	++++
Escherichia coli	GT1659	"	++++	+++	+	+++	++	++++	+++	++
Haemophilus influenza	GT0244	"	++	+++	+	+++	++	++++	+++	++
Haemophilus influenza	ATCC33391	"	ND	ND	ND	+++	+++	+++	+++	+++
Haemophilus ducreyi	GT0243	"	++++	++++	++	ND	++	++++	++++	++
Hafnia alvei	GT0241	"	++++	+++	+	++++	+++	++++	++++	+++
Morganella morganii	GT0303	"	++++	++++	+	++++	++++	++++	+++	+++
Klebsiella pneumoniae	GT1500	"	++++	++++	+	++++	+++	+++	+++	+++
Proteus mirabilis	GT1496	"	++++	++++	+	++++	++++	++++	+++	+++
Providencia alcalifaciens	GT0371	"	++++	++++	+	++++	++++	++++	+++	+++
Pseudomonas aeruginosa	GT1909	"	++++	++++	++	++++	++++	++++	+++	++
Salmonella arizona	GT0799	"	++++	++++	+	++++	+++	++++	+++	++
Salmonella typhimurium	GT0389	"	++++	++++	+	++++	+++	++++	+++	+++
Serratia marcescens	GT0392	"	++++	++++	+	++++	+++	++++	+++	++
Shigella flexneri	GT0798	"	++++	++++	++	++++	++++	++++	++++	++
Vibrio parahaemolyticus	GT0568	"	++++	+++	++	+++	+++	++++	++++	++
Xanthomonas maltophilia	GT0417	"	++++	+++	++	++++	++	++++	++++	++
Yersinia enterocolitica	GT0419	"	++++	++++	++	++++	++++	++++	++++	++++
Alcaligenes faecalis	GT0610	Purple	++++	+++	+	+++	+	+++	+++	++
Branhamella catarrhalis	GT0014	beta	++++	+++	+	++++	++	+++	+++	+++
Chromobacterium violaceum	GT2022	"	++++	++++	+	++++	++++	+++	+++	+++
Kingella indologenes	0246	"	++++	++	+	+++	+++	+++	+++	++
Moraxella osloensis	GT0301	"	++++	+++	+	++++	+++	++++	+++	+++

TABLE 4 (cont'd): DOT BLOT HYBRIDIZATION OF 23S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1512	1256	1398	1600	1601	1602	1596	1597
Morexella phenylpyruvica	GT0302	"	++++	++++	+	++++	++	+++	+++	+++
Neisseria gonorrhoeae	GT0315	"	++++	++++	+	++++	++	++++	++++	++
Neisseria meningitidis	GT0349	"	++++	++++	+	++++	+++	++++	++++	++
Pseudomonas acidovorans	GT0376	"	++++	++++	+	++++	+++	++++	++++	++
Pseudomonas cepacia	GT2015	"	++++	+++	+	++++	+++	++++	+++	++
Rhodocyclus gelatinosa	ATCC17013	"	++++	+++	+	+++	+++	++++	+++	++
Vitreoscilla stercoraria		"	++++	++	+	++++	+++	++++	++++	++++
Achromobacter xerosis	GT0810	Purple	++++	++	+	+++	+++	++++	+++	+++
Acidiphilium cryptum	ATCC33463	alpha	++++	++	+	++++	+++	++++	++++	++++
Agrobacterium tumefaciens	GT2021	"	++++	++	+	++	++	++++	++	+++
Brucella abortus	ATCC23448	"	++++	++++	+	+++	+++	++++	+++	+++
Flavobacterium capsulatm	GT2025	"	++++	+++	+	++++	+++	++++	++	+++
Mycoplana bullata	GT2023	"	++++	+++	+	++++	+++	++++	+++	++++
Pseudomonas diminuta	GT2020	"	++++	+++	+	++++	+++	++++	+++	+++
Rhodobacter sphaeroides	ATCC17023	"	++++	+++	++	++++	+++	++++	+++	+++
Rhodospirillum rubrum	ATCC25903	"	++++	++++	+	++++	+++	++++	+++	+++
Thiobacillus versutus	ATCC25364	"	++++	+++	+	++++	++++	++++	++++	++++
Desulfovibrio desulfuricans	ATCC 7757	delta	++++	+++	+	++++	++++	++++	+	+
Cardiobacterium hominis	GT2095	Gm -	++++	+++	+	++++	+++	++++	++	+++
Francisella tularensis	GT2172	Gm -	++++	+++	+	++++	+++	++++	++++	++++
Campylobacter jejuni	GT0022	Campy	++++	-	++++	+++	++	++++	+++	+++
Campylobacter pylori	GT0026	"	++++	-	+++	++++	+++	++++	+++	+++
Campylobacter sputorum	GT0027	"	++++	-	+++	++++	+++	++++	+++	+++
Bacillus brevis	GT0803	lowG+C	++++	+++	+	++++	+++	++++	+++	+++
Bacillus subtilis	GT0804	Gm +	++++	+++	+	++++	+++	++++	++++	+++
Clostridium clostridioforme	ATCC25537	"	++++	+++	+	+++	++	++++	++++	+++
Clostridium sordellii	GT0567	"	++++	+++	+	+++	+++	++++	++++	+++
Clostridium sporogenes	ATCC 3587	"	++++	+++	+	+++	++	++++	++++	+++
Clostridium histolyticum	ATCC19401	"	++++	+++	+	-	+	++++	++++	++
Clostridium perfringens	ATCC13124	"	++++	-	+	+++	+++	++++	++++	++
Clostridium ramosum	ATCC25582	"	++++	-	+	++	++	++++	++++	++
Kurthia zopfii	ATCC33403	"	++++	++++	+	++++	+++	++++	++++	++
Lactobacillus acidophilus	GT0256	"	++++	+++	+	++++	+++	++++	++++	+++
Lactobacillus plantarum	GT0258	"	++++	+++	+	++++	+++	++++	+++	++

TABLE 4 (cont'd): DOT BLOT HYBRIDIZATION OF 23S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1512	1256	1398	1600	1601	1602	1596	1597
Listeria monocytogenes	IG3299	"	++++	+++	+	++++	+++	++++	++	++++
Mycoplasma pneumoniae	ATCC15531	"	++++	-	+	++	-	-	-	-
Mycoplasma putrefaciens	ATCC15718	"	++++	-	-	+++	++	++++	+++	+++
Peptostreptococcus productus	ATCC27340	"	++++	+++	-	++	++	++++	+++	+++
Planococcus citreus	ATCC14404	"	++++	+++	+	++++	+++	++++	++++	+++
Staphylococcus aureus	GT0399	"	++++	++++	+	++++	+++	++++	++++	+++
Staphylococcus aureus	GT1711	"	++++	+++	+	++++	+++	++++	+++	+++
Staphylococcus epidermidis	GT0401	"	++++	+++	+	++++	+++	++++	+++	+++
Staphylococcus haemolyticus	ATCC29970	"	++++	+++	+	++++	+++	++++	+++	+++
Streptococcus agalactiae	GT0405	"	++++	+++	+	++++	+++	++++	+++	++++
Streptococcus bovis	GT0668	"	++++	++	+	++++	+++	++++	+++	++++
Streptococcus faecalis	GT0406	"	++++	++	+	++++	+++	++++	+++	+++
Streptococcus morbillorum	GT2194	"	++++	+++	+	++	+++	++++	++	++++
Streptococcus mutans	GT0412	"	++++	+++	+	++++	++	++++	+++	+++
Streptococcus pneumoniae	GT0408	"	++++	+++	+	++++	++	++++	+++	+++
Streptococcus salivarius	GT0410	"	++++	+++	+	++++	++	++++	+++	++
Streptococcus sanguis	GT0411	"	ND	ND	+	++++	+++	++++	+++	+++
Bifidobacterium dentium	GT0012	hiG+C	-	+++	+	++++	+++	++++	+++	+++
Corynebacterium genitalium	GT0045	Gm +	++	+++	+	++++	+++	++++	++++	+++
Crynebacterium glutamicum	GT2120	"	++	+++	+	++++	+++	++++	++++	+++
C rynebacterium pseudodiphtheriticum	GT2119	"	++++	+++	+	++++	+++	++++	++++	+++
Corynebacterium pseudotuberculosis	GT2122	"	++++	+++	+	++++	+++	++++	++++	++++
C rynebacterium pyogenes	GT2121	"	++	++	+	++++	++	++++	++++	++++
Corynebacterium xerosis	GT0046	"	+	++	+	+++	++	++++	++	+++
Mycobacterium bovis	BCG	"	+	++	+	+++	+	++++	++	+++
Mycobacterium kansasii		"	+++	+++	+	++++	+++	++++	+++	+++
N cardia asteroides	GT2191	"	++++	+++	+	++++	+++	++++	++++	+++
Rhodococcus rhodochrous		"	++	+++	+	++++	++	++++	++++	+++
Aerococcus viridans	GT2116	Misc	++++	+++	+	++++	++	++++	++++	++++
Fusobacterium necrophorum	GT0238	Gm +	++	+++	+	+++	++	++++	++++	++++
Fusobacterium prausnitzii	ATCC27768	"	++++	+++	+	++++	+++	++++	++++	++++
Gemella haemolysans	GT2118	"	++++	+	+	++++	+++	++++	++++	++++
H liobacillus mobilis		"	++++	+++	+	-	+	++++	++	++++
Phormidium ectocarpi		Cyano	++++	+++	+	+	++	++++	++	++

TABLE 4 (cont'd): DOT BLOT HYBRIDIZATION OF 23S rRNA-TARGETED PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 1512	1256	1398	1600	1601	1602	1596	1597
Plectonema boryanum		"	++++	+++	+	+	+	++++	++	++
Borrelia burgdorferi		Spiro	++++	+++	+	+++	+++	++++	+++	++
Borrelia turicatae		"	++++	++++	+	++++	++++	++++	++++	++
Leptospira interrogans-pomona		"	++++	+++	+	+++	+++	++++	+++	+++
Leptospira biflexa (Patoc-Patoc)		"	++++	+++	+	+++	++	++++	++	++
Leptospira biflexa (CDC)		"	++++	+++	+	+++	++	++++	++	++
Spirochaeta aurantia		"	++++	++++	+	+++	++++	++++	++	++
Bacteroides fragilis	25285	Bact	++++	+++	+	+++	++	++++	++	++
Bacteroides fragilis	29771	"	++++	+++	+	+++	++	++++	+++	++
Bacteroides thetaiotaomicron	0572	"	++++	+++	+	+	+	++++	++	++
Bacteroides melaninogenicus	0011	"	++++	+++	+	+	++	++++	+++	+
Flavobacterium meningosepticum	0237	"	++++	++++	+	++++	++++	++++	++++	+
Chlamydia psittaci	-	Chlam	-	+++	-	++++	++++	+++	++	++
Chlamydia trachomatis	LGV	"	-	+++	-	++++	+++	++++	++	+
Chlorobium limicola		Misc.	++++	++++	+	++++	++++	++++	+	++
Chloroflexus aurantiacus	Y400	"	++	+++	+	++	++	++++	++	++
Deinococcus radiodurans	2608	"	++++	++++	+	++++	++++	++++	+	++
Planctomyces maris	2577	"	++++	+++	+	++++	++++	++++	+++	-
Normal Stool RNA			++++	+++	-	+++	+++	++++	++	++
Mouse L-Cell			-	-	-	-	-	-	-	-
Wheat Germ			-	-	-	-	-	-	-	-
Normal Human Blood			-	-	-	-	-	-	-	-
Candida lusitaniae	403-87		+	-	-	-	-	-	-	-
Candida parapsilosis	882-88		+	-	-	-	-	-	-	-
Candida tropicalis	224-87		+	-	-	-	-	-	-	-
Candida albicans	1008-88		+	-	-	-	-	-	-	-
Candida albicans	223-87		+	-	-	-	-	-	-	-
Candida albicans	819-88		+	-	-	-	-	-	-	-

* Inclusivity and Exclusivity data was determined after overnight exposures.
** Each organism is represented by 100ng of CsTFA purified RNA. ++++ = positive level of hybridization, + = barely detectable and - = zero, ND - not done.

TABLE 5: DOT BLOT HYBRIDIZATION - GRAM POSITIVE & GRAM NEGATIVE PROBES

			PROBE HYBRIDIZATION								
			16S RNA-TARGET			23S RNA-TARGET					
Genus species	strain	div	1744	1745	1746	1657	1656	1598	1599	1595
Acinetobacter calcoaceticus	GT0002	Purple	-	-	-	++++	-	++	-	++++
Aeromonas sobria	GT0007	gamma	-	-	-	++++	-	++	+	++++
Alteromonas putrefaciens	GT1945	"	-	-	-	++++	-	++++	-	++++
Citr bacter amalonaticus	GT0690	"	-	-	-	++++	-	++++	-	++++
Citrobacter diversus	GT0030	"	-	-	-	++++	-	++++	-	++++
Citr bacter freundii	GT0687	"	-	-	-	++++	-	++++	-	++++
Edwardsiella tarda	GT0569	"	-	-	-	++++	-	++++	-	++++
Enterobacter agglomerans	GT0683	"	-	-	-	++++	-	++	-	++++
Enterobacter cloacae	GT0686	"	+	+	-	++++	-	++	+	++++
Enterobacter sakazakii	GT0062	"	-	-	-	++++	-	++++	-	++++
Escherichia coli	GT1665	"	-	-	-	++++	-	++++	-	++++
Escherichia coli	GT1592	"	-	-	-	++++	-	++++	-	++++
Echerichia coli	GT1659	"	-	-	-	++++	+	++	+	++++
Haemophilus influenza	ATCC33391	"	-	-	-	++++	++++	++++	-	++++
Haemophilus ducreyi	GT0243	"	-	-	-	++++	-	++++	-	++++
Hafnia alvei	GT0241	"	-	-	-	++++	-	++++	+	+++
Morganella morganii	GT0303	"	-	-	-	++++	-	++++	-	+++
Klebsiella pneumoniae	GT1500	"	-	-	-	++++	-	++++	-	++
Pr teus mirabilis	GT1496	"	-	-	-	++++	-	++++	+	+++
Pr videncia alcalifaciens	GT0371	"	-	-	-	++++	-	++	+	+++
Pseudomonas aeruginosa	GT1909	"	-	-	-	++++	-	++	+	++++
Salmonella arizona	GT0799	"	-	-	-	++++	-	++	+	++++
Salmonella typhimurium	GT0389	"	-	-	-	++++	-	++++	-	++++
Serratia marcescens	GT0392	"	-	-	-	++++	-	++++	-	+++
Shigella flexneri	GT0798	"	-	-	-	++++	-	++++	-	+++
Vibrio parahaemolyticus	GT0568	"	-	-	-	++++	-	++++	+	+++
Xanth monas maltophilia	GT0417	"	-	-	-	+	+	++++	+	+++
Yersinia enterocolitica	GT0419	"	-	-	-	++++	-	++++	+	++++
Alcaligines faecalis	GT0610	Purple	-	-	-	-	++++	++++	-	+++
Branhamella catarrhalis	GT0014	beta	-	-	-	++++	-	++++	-	+++
Chr mobacterium violaceum	GT2022	"	-	-	-	++++	+++	++++	+	+++
Kingella indologenes	0246	"	-	-	-	++++	-	+++	-	+++
Moraxella osloensis	GT0301	"	-	-	-	++++	-	++++	+	+
M rexella phenylpyruvica	GT0302	"	-	-	-	++++	-	++++	-	++++

TABLE 5: (cont'd) DOT BLOT HYBRIDIZATION - GRAM POSITIVE & GRAM NEGATIVE PROBES

			PROBE HYBRIDIZATION							
			16S RNA-TARGET			23S RNA-TARGET				
Genus species	strain	div	1744	1745	1746	1657	1656	1598	1599	1595
Borrelia burgdorferi		Spiro	-	+	+++	-	++++	++	-	-
Borrelia turicatae		"	-	++	++++	-	++++	++++	-	+
Leptospira interrogans-pomona		"	-	+	-	-	++++	++++	++	+
Leptospira biflexa (Patoc-Patoc)		"	-	-	-	-	++++	++++	++	+
Leptospira biflexa (CDC)		"	-	-	-	-	++++	+++	++	+
Spirochaeta aurantia		"	++++	-	-	-	++++	++	++++	+
Bacteroides fragilis	25285	Bact	++++	-	-	-	-	-	++++	+
Bacteroides fragilis	29771	"	++++	-	-	-	-	-	++++	+
Bacteroides thetaiotaomicron	0572	"	+	-	-	-	-	-	++++	+
Bacteroides melaninogenicus	0011	"	++++	-	-	-	-	-	++++	+
Flavobacterium meningosepticum	0237	"	++++	-	-	-	+	-	+++	-
Chlamydia psittaci		Chlamy	-	-	-	-	-	+	+	++
Chlamydia trachomatis	LGV	"	-	-	-	-	-	++	++	++
Chlorobium limicola		Misc	++++	-	-	-	+++	-	-	-
Chloroflexus aurantiacus	Y400	"	++++	-	-	-	+++	-	++++	+++
Deinococcus radiodurans	2608	"	+++	-	-	-	+++	-	++++	+
Planctomyces maris	2577	"	-	-	-	-	-	-	-	-
Normal Stool RNA			+++	++++	++	++	+++	+	+++	++
Mouse L-Cell			-	-	-	-	-	-	-	-
Wheat Germ			-	-	-	-	-	-	-	-
Normal Human Blood			-	-	-	-	-	-	-	-
Candida lusitaniae	403-87		-	-	-	-	-	-	-	-
Candida parapsilosis	882-88		-	-	-	-	-	-	-	-
Candida tropicalis	224-87		-	-	-	-	-	-	-	-
Candida albicans	1008-88		-	-	-	-	-	-	-	-
Candida albicans	223-87		-	-	-	-	-	-	-	-
Candida albicans	819-88		-	-	-	-	-	-	-	-

* Inclusivity and Exclusivity data was determined after overnight exposures.
** Each organism is represented by 100ng of CsTFA purified RNA.
*** ++++ = positive level of hybridization, + = barely detectable and - = zero. Probe 1746 was hybridized at 37 C and washes at 50 C.

TABLE 5: (cont'd) DOT BLOT HYBRIDIZATION - GRAM POSITIVE & GRAM NEGATIVE PROBES

			PROBE HYBRIDIZATION							
			16S RNA-TARGET			23S RNA-TARGET				
Genus species	strain	div	1744	1745	1746	1657	1656	1598	1599	1595
Mycoplasma pneumoniae	ATCC15531	"	-	++++	++++	-	-	-	-	++++
Mycoplasma putrefaciens	ATCC15718	"	-	++++	+++	-	-	-	++++	-
Peptostreptococcus productus	ATCC27340	"	++++	++++	++++	-	+	-	++++	-
Planococcus citreus	ATCC14404	"	++++	++++	++++	-	++++	+	++++	-
Staphylococcus aureus	GT0399	"	++++	++++	++++	-	++++	+	++++	-
Staphylococcus aureus	GT1711	"	++++	++++	++++	-	++++	+	++++	-
Staphylococcus epidermidis	GT0401	"	++++	++++	++++	-	++++	+	++++	-
Staphylococcus haemolyticus	ATCC29970	"	++++	++++	++++	-	++++	+	++++	-
Streptococcus agalactiae	GT0405	"	++++	++++	++++	-	++++	-	++++	-
Streptococcus bovis	GT0668	"	++++	++++	++++	-	++++	-	++++	-
Streptococcus faecalis	GT0406	"	++++	++++	++++	-	++++	-	++++	-
Streptococcus morbillorum	GT2194	"	++++	++++	+++	-	++++	+	++++	-
Streptococcus mutans	GT0412	"	++++	++++	+++	-	++++	-	++++	-
Streptococcus pneumoniae	GT0408	"	++++	++++	++++	-	++++	-	++++	-
Streptococcus salivarius	GT0410	"	++++	++++	++++	-	++++	-	++++	-
Streptococcus sanguis	GT0411	"	++++	++++	++++	-	++++	-	++++	-
Bifidobacterium dentium	GT0012	hiG+C	-	++++	+++	++++	-	-	++++	+
Corynebacterium genitalium	GT0045	Gm +	++++	++++	++++	++++	+	-	++++	+
Crynebacterium glutamicum	GT2120	"	++++	++++	++++	++++	-	-	++++	+
Corynebacterium pseudodiphtheriticum	GT2119	"	++++	++++	++++	-	++++	+	++++	-
Corynebacterium pseudotuberculosis	GT2122	"	++++	++++	++++	-	+++	-	++++	-
Corynebacterium pyogenes	GT2121	"	++++	++++	++++	-	-	+	++++	+++
Corynebacterium xerosis	GT0046	"	++++	++++	++	++++	-	-	++++	+
Mycobacterium bovis	BCG	"	++++	++++	-	++++	-	-	++++	+
Mycobacterium kansasii		"	++++	++++	++	++++	-	-	++++	+
Nocardia asteroides	GT2191	"	++++	-	-	-	-	++++	+++	++
Rhodococcus rhodochrous		"	++++	++++	+	++++	-	-	++++	+
Aerococcus viridans	GT2116	Misc	++++	++++	++++	-	++	++	++++	-
Fusobacterium necrophorum	GT0238	Gm +	++++	++++	++	+++	-	++	++++	-
Fusobacterium prausnitzii	ATCC27768	"	++++	++++	++	++	-	+	++++	-
Gemella haemolysans	GT2118	"	++++	++++	++++	-	++++	++++	++++	-
Heliobacillus mobilis		"	++++	++++	+++	-	++++	-	++++	-
Phormidium ectocarpi		Cyano	++++	++++	++	-	-	-	++++	-
Plectonema boryanum		"	++++	++++	-	-	+	-	++++	-

TABLE 5: (cont'd) DOT BLOT HYBRIDIZATION - GRAM POSITIVE & GRAM NEGATIVE PROBES

Genus species	strain	div	PROBE HYBRIDIZATION 16S RNA-TARGET 1744	1745	1746	23S RNA-TARGET 1657	1656	1598	1599	1595
Neisseria gonorrhoeae	GT0315	"	-	-	-	++++	++++	++++	-	++++
Neisseria meningitidis	GT0349	"	-	-	-	++++	++++	++++	-	+++
Pseudomonas acidovorans	GT0376	"	-	-	-	++++	++++	++++	-	+++
Pseudomonas cepacia	GT2015	"	-	-	-	++	++++	++++	-	+++
Rhodocyclus gelatinosa	ATCC17013	"	-	-	-	-	-	++++	-	+++
Vitreoscilla stercoraria		"	-	-	-	-	++++	+++	-	++
Achromobacter xerosis	GT0810	Purple	-	-	-	++++	++++	++++	-	++
Acidiphilium cryptum	ATCC33463	alpha	-	-	-	+++	-	-	-	-
Agrobacterium tumefaciens	GT2021	"	++	-	-	++++	-	++++	++	++
Brucella abortus	ATCC23448	"	++	-	-	++++	-	++++	+++	+++
Flavobacterium capsulatum	GT2025	"	+	-	-	++++	-	++	++	-
Mycoplana bullata	GT2023	"	-	-	-	++++	-	++	-	-
Pseudomonas diminuta	GT2020	"	-	-	-	++++	-	+++	-	+
Rhodobacter sphaeroides	ATCC17023	"	-	-	-	++++	-	+++	-	++
Rhodospirillum rubrum	ATCC25903	"	++++	-	-	++++	-	+	+	+++
Thiobacillus versutus	ATCC25364	"	++	-	-	++++	-	+++	-	++
Desulfovibrio desulfuricans	ATCC 7757	delta	-	-	-	-	-	+++	-	++
Cardiobacterium hominis	GT2095	Misc	-	-	-	++++	-	+++	-	+
Francisella tularensis	GT2172	Gm -	-	-	-	++++	-	+++	-	++++
Campylobacter jejuni	GT0022	Campy	-	-	-	-	++++	+++	++	-
Campylobacter pylori	GT0026	"	-	-	-	-	++++	++++	++	+
Campylobacter sputorum	GT0027	"	-	-	-	-	++	++++	++	-
Bacillus brevis	GT0803	lowG+C	++++	++++	++++	-	++++	+	++++	-
Bacillus subtilis	GT0804	Gm +	++++	++++	++++	-	++++	+	++++	-
Clostridium clostridioforme	ATCC25537	"	++++	++++	++++	-	++++	-	++++	-
Clostridium sordellii	GT0567	"	++++	++++	++++	-	++++	-	++++	-
Clostridium sporogenes	ATCC 3587	"	++++	++++	++++	-	++++	-	++++	-
Clostridium histolyticum	ATCC19401	"	++++	++++	++++	-	++++	-	++++	-
Clostridium perfringens	ATCC13124	"	++++	++++	++++	-	++++	-	++++	-
Clostridium ramosum	ATCC25582	"	++++	++++	++++	-	-	-	++++	+
Kurthia zopfii	ATCC33403	"	++++	++++	++++	-	++++	-	++++	-
Lactobacillus acidophilus	GT0256	"	++++	++++	++++	-	+++	-	++++	-
Lactobacillus plantarum	GT0258	"	++++	++++	++++	-	+++	+	++++	-
Listeria monocytogenes	IG3299	"	++++	++++	++++	-	+++	-	++++	-

What is claimed is:

1. A nucleic acid fragment capable of hybridizing to rRNA or rDNA of eubacteria.

2. The nucleic acid fragment of claim 1 wherein said fragment is not capable of hybridizing to rRNA or rDNA of Mouse L cells, wheat germ, human blood or Candida albicans.

3. The nucleic acid fragment of claim 2, wherein said fragment is complementary to at least 90% of a sequence comprising any ten consecutive nucleotides within probes selected from the group consisting of 1638, 1642, 1643, 1738, 1744, 1659, 1660, 1661, 1739, 1740, 1741, 1742, 1745, 1746, 1743, 1637, 1639, 1640, 1641, 1730, 1731, 1658, 1656, 1657, 1653, 1654, 1655, 1651, 1652, 1512, 1256, 1398, 1511, 1595, 1600, 1601, 1602, 1598, 1599, 1596, 1597.

4. The nucleic acid fragment of claim 2, wherein said fragment is homologous to at least 90% of a sequence comprising any ten consecutive nucleotides within probes selected from the group consisting of 1638, 1642, 1643, 1738, 1744, 1659, 1660, 1661, 1739, 1740, 1741, 1742, 1745, 1746, 1743, 1637, 1639, 1640, 1641, 1730, 1731, 1658, 1656, 1657, 1653, 1654, 1655, 1651, 1652, 1512, 1256, 1398, 1511, 1595, 1600, 1601, 1602, 1598, 1599, 1596, 1597.

5. A set of probes comprising at least two nucleic acids fragments, at least one of which is selected from the group consisting of 1638, 1642, 1643, 1738, 1744, 1659, 1660, 1661, 1739, 1740, 1741, 1742, 1745, 1746, 1743, 1637, 1639, 1640, 1641, 1730, 1731, 1658, 1656, 1657, 1653, 1654, 1655, 1651, 1652, 1512, 1256, 1398, 1511, 1595, 1600, 1601, 1602, 1598, 1599, 1596, 1597 and their complementary sequences.

6. The nucleic acid fragment of claim 1 which is probe 1638 or its complementary sequence.

7. The nucleic acid fragment of claim 1 which is probe 1642 or its complementary sequence.

8. The nucleic acid fragment of claim 1 which is probe 1643 or its complementary sequence.

9. The nucleic acid fragment of claim 1 which is probe 1738 or its complementary sequence.

10. The nucleic acid fragment of claim 1 which is probe 1744 or its complementary sequence.

11. The nucleic acid fragment of claim 1 which is probe 1659 or its complementary sequence.

12. The nucleic acid fragment of claim 1 which is probe 1660 or its complementary sequence.

13. The nucleic acid fragment of claim 1 which is probe 1661 or its complementary sequence.

14. The nucleic acid fragment of claim 1 which is probe 1739 or its complementary sequence.

15. The nucleic acid fragment of claim 1 which is probe 1740 or its complementary sequence.

16. The nucleic acid fragment of claim 1 which is probe 1741 or its complementary sequence.

17. The nucleic acid fragment of claim 1 which is probe 1742 or its complementary sequence.

18. The nucleic acid fragment of claim 1 which is probe 1745 or its complementary sequence.

19. The nucleic acid fragment of claim 1 which is probe 1746 or its complementary sequence.

20. The nucleic acid fragment of claim 1 which is probe 1743 or its complementary sequence.

21. The nucleic acid fragment of claim 1 which is probe 1637 or its complementary sequence.

22. The nucleic acid fragment of claim 1 which is probe 1639 or its complementary sequence.

23. The nucleic acid fragment of claim 1 which is probe 1640 or its complementary sequence.

24. The nucleic acid fragment of claim 1 which is probe 1641 or its complementary sequence.

25. The nucleic acid fragment of claim 1 which is probe 1730 or its complementary sequence.

26. The nucleic acid fragment of claim 1 which is probe 1731 or its complementary sequence.

27. The nucleic acid fragment of claim 1 which is probe 1658 or its complementary sequence.

28. The nucleic acid fragment of claim 1 which is probe 1656 or its complementary sequence.

29. The nucleic acid fragment of claim 1 which is probe 1657 or its complementary sequence.

30. The nucleic acid fragment of claim 1 which is probe 1653 or its complementary sequence.

31. The nucleic acid fragment of claim 1 which is probe 1654 or its complementary sequence.

32. The nucleic acid fragment of claim 1 which is probe 1655 or its complementary sequence.

33. The nucleic acid fragment of claim 1 which is probe 1651 or its complementary sequence.

34. The nucleic acid fragment of claim 1 which is probe 1652 or its complementary sequence.

35. The nucleic acid fragment of claim 1 which is probe 1512 or its complementary sequence.

36. The nucleic acid fragment of claim 1 which is probe 1256 or its complementary sequence.

37. The nucleic acid fragment of claim 1 which is probe 1398 or its complementary sequence.

38. The nucleic acid fragment of claim 1 which is probe 1511 or its complementary sequence.

39. The nucleic acid fragment of claim 1 which is probe 1595 or its complementary sequence.

40. The nucleic acid fragment of claim 1 which is probe 1600 or its complementary sequence.

41. The nucleic acid fragment of claim 1 which is probe 1601 or its complementary sequence.

42. The nucleic acid fragment of claim 1 which is probe 1602 or its complementary sequence.

43. The nucleic acid fragment of claim 1 which is probe 1598 or its complementary sequence.

44. The nucleic acid fragment of claim 1 which is probe 1599 or its complementary sequence.

45. The nucleic acid fragment of claim 1 which is probe 1596 or its complementary sequence.

46. The nucleic acid fragment of claim 1 which is probe 1597 or its complementary sequence.

47. A method of detecting the presence of eubacteria in a sample comprising:

a) contacting said sample with at least one nucleic acid fragment under conditions that allow said fragment to hybridize to rRNA or rDNA of said eubacteria, if present in said sample, to form hybrid nucleic acid complexes not to rRNA or rDNA of non-eubacteria; and

b) detecting said hybrid nucleic acid complexes as an indication of the presence of said eubacteria in said sample.

48. The method of claim 47 wherein said nucleic acid fragment of said contacting step is selected from the group of probes consisting of 1638, 1642, 1643, 1738, 1744, 1659, 1660, 1661, 1739, 1740, 1741, 1742, 1745, 1746, 1743, 1637, 1639, 1640, 1641, 1730, 1731, 1658, 1656, 1657, 1653, 1654, 1655, 1651, 1652, 1512, 1256, 1398, 1511, 1595, 1600, 1601, 1602, 1598, 1599, 1596, 1597.

49. The method of claim 47 wherein said eubacteria are gram-positive and said nucleic acid fragment is selected from the group of probes consisting of 1599, 1656, 1744, 1745 and 1746.

50. The method of claim 47 wherein said eubacteria are gram-negative and said nucleic acid fragment is selected from the group of probes consisting of 1599, 1656, 1744, 1745 and 1746.

51. The method of claim 47 wherein said contacting step involves a nucleic acid fragment selected from the group consisting of probe 1638, probe 1642 and probe 1643 and said detecting step involves further contacting said sample with a second nucleic acid fragment selected from the group of probes consisting of 1637, 1639, 1640 and 1641 and amplifying eubacterial 16S rRNA or 16S rRNA gene sequences by the polymerase chain reaction.

FIGURE 1: THE THREE KINGDOMS

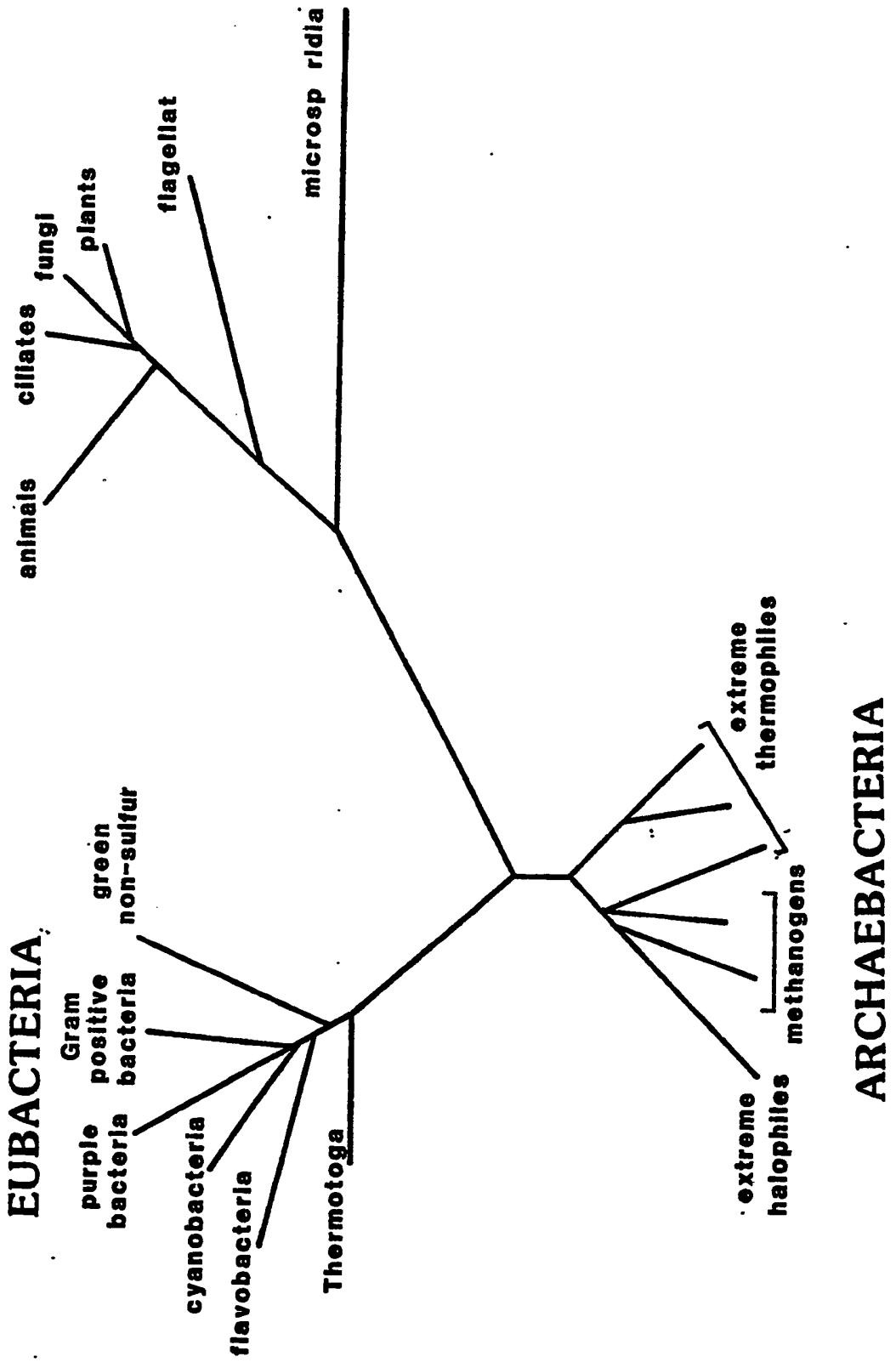
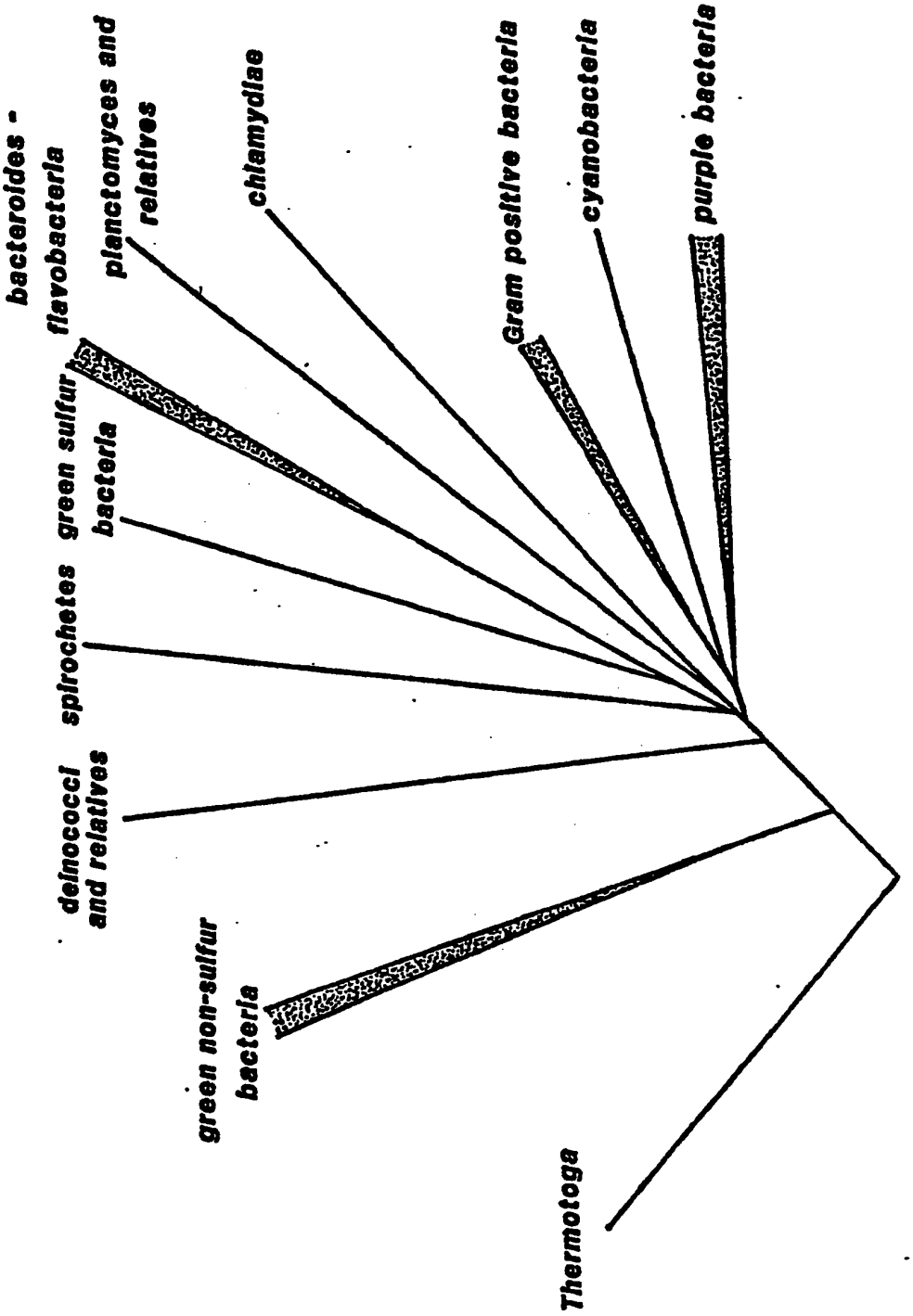


FIGURE2: THE EUBACTERIAL KINGDOM



INTERNATIONAL SEARCH REPORT

International Application No PCT/US 90/03004

I. CLASSIFICATION F SUBJECT MATTER (if several classification symbols apply, indicate all)[6]

According to International Patent Classification (IPC) or to both National Classification and IPC

IPC5: C 12 Q 1/68

II. FIELDS SEARCHED

Minimum Documentation Searched[7]

Classification System	Classification Symbols
IPC5	C 12 Q; C 07 H

Documentation Searched other than Minimum Documentation to the Extent that such Documents are included in Fields Searched[8]

III. DOCUMENTS CONSIDERED TO BE RELEVANT[9]

Category *	Citation of Document,[11] with indication, where appropriate, of the relevant passages[12]	Relevant to Claim No.[13]
X Y	EP, A1, 0245129 (INSTITUT PASTEUR) 11 November 1987, see especially the abstract	1-5,21, 47,48, 51, 3-5,21, 51
X Y	EP, A1, 0250662 (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 7 January 1988, see the whole document	1,2, 47 3-5,21, 48,51
A	EP, A1, 0277237 (TORAY INDUSTRIES, INC.) 10 August 1988, see the whole document	1-51

* Special categories of cited documents:[10]

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

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"X" document of particular relevance, the claimed invention cannot be considered novel or cannot be considered to involve an inventive step

"Y" document of particular relevance, the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

IV. CERTIFICATION

Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report
28th September 1990	17. 10. 90
International Searching Authority	**Signature of Authorized Officer**
EUROPEAN PATENT OFFICE	H. Ballesteros

Form PCT/ISA/210 (second sheet) (January 1985)

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FR M THE SECOND SHEET)

Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No
X	SCIENCE, Vol. 243, March 1989, Edward F. DeLong et al.: "Phylogenetic Stains: Ribosomal RNA-Based Probes for the Identification of Single Cells ", see page 1360	1,2, 47
Y		3-5,21, 48,51
	--	
X	Dialog Informational Service, file 154: Medline 83-90, accession no. 06930668, Medline accession no. 89232668, Chen K. et al: "Broad range DNA probes for detecting and amplifying eubacterial nucleic acids", & FEMS Microbiol Lett Jan 1 1989, 48(1) p19-24	1,2
Y		3-5,21, 48,51
	--	
X	Dialog Information Service, file 154: Medline 83-90, accession no. 06470172, Medline accession no. 88115172, Giovannoni S.J. et al: "Phylogenetic group-specific oligodeoxynucleotide probes for identification of single microbial cells", & J Bacteriol (UNITED STATES) Feb 1988, 170 (2) p720-6	1
Y		3-5,21, 48,51
	--	

ANNEX TO THE INTERNATIONAL SEARCH REPORT ON INTERNATIONAL PATENT APPLICATION NO. PCT/US 90/03004

SA 38253

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.
The members are as contained in the European Patent Office EDP file on 28/08/90
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Patent document cited in search report	Publication date	Patent family member(s)		Publication date
EP-A1- 0245129	11/11/87	AU-D-	7232587	20/10/87
		FR-A-B-	2596774	09/10/87
		JP-T-	1500001	12/01/89
		WO-A-	87/05907	08/10/87
EP-A1- 0250662	07/01/88	NONE		
EP-A1- 0277237	10/08/88	WO-A-	88/00618	28/01/88

For more details about this annex : see Official Journal of the European patent Office, No. 12/82

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